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Result
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Maximum DB seq
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1154
1166
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                                                                                                                                                                                                          and is derived by analysis of the total score distribution.
423
422.4
418.8
410.6
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391.2
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13736207 seqs, 6748477542 residues
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Gapop 10.0 , Gapext 1.0
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1807
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                                                                                                                                                                                                                                                                                                                                                                                                                        Maximum Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              April 28, 2002, 16:44:30 ; Search time 1502.78 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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em_gss_inv:*
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gb_htc:*
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1627
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AL518877
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BH600970
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BG596023
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                                                                                                                                                                                          SUMMARIES
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16229.254 Million cell updates/sec
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    BG368908 HVSME1002
BE053804 GA_EA003
AL531607 AL531607
AW395525 $128h04 y
AW308961 $f92d04 y
AL558916 AL558916
BB611086 BB611086
                                                                                                                BC013141 Homo sapi
BH600970 BOGCN27TR
BE558877 HV_CEb002
BI118849 EST237 Di
                                                                     AI994124 701499210
AL518877 AL518877
                                                                                                                                                              Description
                                                                                      BG596023 EST494689
BG594704 EST493382
W433397 22774 CD4-1
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45	44	43	42	41	40	39	38	37	36	35	34	(L)	32	ω	30	29	28	27	26	25	24	23	22	21	20	19	18
342.2	342.2	343.2	343.2	344.8	345	346	347	349.2	352.8	353.2	353.8	360	361	363.4	365.2	369.6	372	372	372.8	373.4	374.2	374.8	377.2	377.6	378.8	378.8	380.6
18.9	18.9	19.0	19.0	19.1	19.1	19.1	19.2	19.3	19.5	19.5	19.6	19.9	20.0	20.1	20.2	20.5	20.6	20.6	20.6	20.7	20.7	20.7	20.9	20.9	21.0	21.0	21.1
878	643	871	722	528	345	603	890	650	1034	998	910	737	636	910	765	637	1007	905	977	882	988	898	437	696	986	613	1030
10	9	10	10	9	9	10	9	10	10	9	9	10	10	10	9	9	10	10	12	10	10	9	10	10	9	10	12
BF631408	AW616696	BE747628	BG914796	A1736699	AV536771	BE517647	AL527966	BG598526	BM461585	AL555361	AL546378	BI177518	BI075248	BG756668	AJ394397	AW686294	BM452740	BI855025	CNS072YS	BG367319	BM468325	AL541430	R90034	BG597901	AL536160	BG521741	CNS06MLI
BF631408 HVSMEb001	AW616696 EST323107	BE747628 601577573	BG914796 602813602	A1736699 sb32d06.y	AV536771 AV536771	BE517647 WHE0801_F	AL527966 AL527966	BG598526 EST503426	BM461585 AGENCOURT	AL555361 AL555361	AL546378 AL546378	BI177518 EST518463	в1075248 IP1_17_н0	BG756668 602715527	AJ394397 AJ394397	AW686294 NF036C08N	BM452740 AGENCOURT	BI855025 603382030	AL426842 clone BAO	BG367319 HVSME1001	BM468325 AGENCOURT	AL541430 AL541430	R90034 16389 Lambd	BG597901 EST496579	AL536160 AL536160	BG521741 13-95 Ste	AL405628 T3 end of

ALIGNMENTS

SOURCE ORGANISM DEFINITION ACCESSION RESULT BC013141 FEATURES COMMENT REFERENCE VERSION KEYWORDS rocus JOURNAL REMARK TITLE AUTHORS Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 28 Row: d Column: 21 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557640 This clone has the following problem: incomplete processing. Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: Baylor College of Medicine Human
Sequencing Center Direct Submission
Direct Submission
Submitted (27-AUG-2001) National Institutes of Health, Mammalian Submitted (27-AUG-2001) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Genomics Office, Nati Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: vilialon@bcm.tmc.edu. Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W., Muzny,D.M., Gibbs,R.A. NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk BC013141 1627 bp Homo sapiens, clone IMAGE:4475960, Strausberg, R. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homo sapiens BC013141.1 GI:15341911 BC013141 Center code: BCM-HGSC (bases 1 to 1627) Location/Qualifiers **MRNA** mRNA Consortium (LLNL) Genome HTC 29-AUG-2001

BB611086

BF632187

AW396525

AW308961

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BASE COUNT
ORIGIN
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978 aggitgcitcaatcittcaatcaaaggicatgcigagigcgicaaatttaigagaicgtt
                                                                                      918
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                                             GTATCAACCTAGTGCTGGTATTACAGTGTGGTGCAGACTCATTATCTGGTGATAGACT
                                                                tttccgaccaggggctgtggtattgcaatgtggtgctgactccctatctggggatcggtt 977
                                                                                                                             TATAGATGATGAGTCATATGGGCAGATATTTAAGCCTATTATCTCAAAGGTGATGGAGAT
                                                                                                                                                    aatcgatgatgagagctatcatctgttattcaagcccatcatggggaaagttatggaaat
                                                                                                                                                                                                                                                                                              TCGTGTAATGACGGTATCATTCCATAAATATGGGGAATACTTTCCTGGCACAGGAGACTT
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/db_xref="taxon:9606"
/clone="IMACE:4475960"
/tissue_type="Prostate, ad
/clone_lib="NIH_MGC_91"
/lab_host="DH10B"
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Pred. No. 2e-117;
0; Mismatches 450;
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TITLE
Query Match
Best Local Similarity
Matches 551; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
Other_GSSs: BOGCN27TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 774)
1 (bases 1 to 774)
1 (coun,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOGCN27TR BOGC
                                                                                                                                                                                                                                                                                                                                       Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica oleracea
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                                                                                               /clone_lib_BOGG"
/clone_lib_BOGG"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
194 c 174 g 184 t
                                                                                                                                                                                  /db_xref="taxon:3712"
/clone="BOGCN27"
                                                                                                                                                                                                                         /organism-"Brassica
/strain-"TO1000DH3"
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                 26.8%;
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               Score 484.2; DB 12; Pred. No. 5.2e-112;
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                      Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, US Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                          1 (bases 1 to 819)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                      Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Snermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                            Contact: Wing RA
                                                                                                                                                                                  Unpublished (2001)
                                                                                                                                                                                                           for barley genomics: Blumeria infected incompatible (Mla6) seedling leaf cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta;
; Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE558877 819 bp mRNA linear EST 23-OCT-2001
HY_CEDD0020K09f Hordeum vulgare seedling green leaf EST library
HYCDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
HY_CED0020K09f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE558877.1 GI:9823367
Email: rwing@clemson.edu
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TGAAGCCGCACCGCATCCGCATGACCCACTCGCTGCTGGCGCAGTACGGCCTCCTCGACC 60
                                                                                                                                                                                                                                                                acgactatgtctcttttctccgcagcattacccctgaaacccagcaagatcagattcgcc
                         ACATCGCCATCAACTGGTCAGGGGGCCTGCACCATGCTAAGAAGTGCGAGGCCTCAGGCT
                                                                                                                                                                                                                                    CCCTCAAGCGCTTCAACGTCGGCGAGGACTGCCCCGTCTTCGACGGCCTCTACAGCTTCT
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of Blumeria graminis f. sp. hordel, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Alsc see Close TJ, Wing R, Kleinhoffs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)* a 239 c 216 g 191 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      green seedlings were challenged with isolate 5874 (AvrMla6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.I. 16151 (Mla6) plants were greenhouse grown Wise lab at Iowa State University, Ames, IA; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                library HVcDNA0005 (Blumeria challenged)"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Hordeum vulgare"
/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="HV_CEb0020K09f"
/clone_lib="Hordeum vulgare seedling green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: xho1;
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74.9%;
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Pred. No. 4.7e-106;
0; Mismatches 202;
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BI118849
BI118849.1
EST.
                                                                                                                                                                                                                                                                                                                                          Song, F.M. and Goodman, R.M. Molecular cloning of differentially expressed systemic acquired resistance in rice Unpublished (2001)
Contact: Song, F.M.; Goodman, R.M.
                                                                                                                                                  BTH-downregulated
Insert Length: 917 Std Error: 0.00
Seq primer: M13 Forward and reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                            Department of Plant Pathology
University of Wisconsin-Madison
Rm 689, Russell Laboratories, 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BI118849 917 bp mRNA linear EST 26-JUN-2001 EST237 Differentially expressed cDNA libraries of BTH-treated/blast fungus-infected rice leaf tissues Oryza sativa cDNA clone HNBN-w14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poathentroldeae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa.
Oryza sativa
                                                                                                                                                                                                                         Email: fmsong@plantpath.wisc.edu;
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                                                                                                                                                                                                                                           608 262 9162
608 262 8643
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/clone_lib-"Differentially expressed cDNA libraries BTH-treated/blast fungus-infected rice leaf tissues" /tissue_type-"Seedling leaves"
                                                                                   /cultivar="Yuanfengzao (a susceptible variety blast disease)"
                                                   /db_xref="taxon:4530"
/clone="HNBN-w14"
                                                                                                                      /organism-"Oryza sativa"
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                                                                                              atggaaattttccgaccaggggctgtggtattgcaatgtggt--gctgactccctatctg
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                                                                       GTGATCGGTTGGGCTGCTTCAACCCTATCGATCAGGGGCCACGCGGAATGTGTGAGATTC
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BTH treatment. Leaf samples were collected twenty-four
hour after inoculation and mRNAs were used for
construction of the differentially expressed cDNA
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Pred. No. 7.5e-104;
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Cathy Ronning
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,
Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
Generations of ESTs from sprouting potato eyes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG596023
BG596023.1 GI:13614151
EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone info: please contact Research Genetics, Libraries Division tel 1-800-711-6195, email cdna@resgen.com Seg primer: M13F-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 760)
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Solanum tuberosum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     198
                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhOI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4113"
/clone="cSTS12024"
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/cultivar="Kennebec"
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76.0%;
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                                                                                                                                                                                                                                                                                                                                             Length 760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B Generations of ESTs from sprouting potato eyes Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  potato.
Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Cathy Ronning
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

1 (bases 1 to 749)
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BG594704
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                                                                                                                                                                                                                                                                                                                                                                             Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                     For clone info:
                                                                                                                                                                                                                                                                                                                                                         primer: M13F-R
196
Ø
               ANOL: Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubers were incubated at 26C in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from tubers.
                                                                                                                                                                                                                            /organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="cSTS8A2"
                                                                                                                                               /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                      /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                            /clone_lib="cSTS"
                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                 please contact Research Genetics, Libraries
O
190
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                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 ttgitattictatgacccigaggicggcaattactatggccaaggicatcccatgaa 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 23.4%;
Local Similarity 76.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCTGTAAATTGGGCTGGTGGATTGCATCATGCCAAGAAATGTGAAGCATCTGGTTTCTG
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                                                                                                                                                                                                                            W43397
                     1 (bases 1 to 535)
Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H.,
L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomashow,M.,
E. and Somerville,C.
                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                   Arabidopsis thaliana
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   summary of
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Pred. No. 1.8e-96;
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                                                                                                                                              gagatcatcgcagcttctcctccgaccatttgactgcgactgtgattacaaccaccgtt 121
                                                                                                                                                                                                                                             GATCCTACGAAAAAGAGGTAATGGATACTGGCGGCAATTCGCTGGCGTCCGGACCTGATG
                            gatcctacgaaaaagaggtaatggatactggcggcaattcgctggcgtccggacctgatg 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 517-353-9168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lansing, Mi
Tel: 517-353-0854
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                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment and EcoRI/NotI adapters (Pharmacla) were ligated to each end. The cDNA was purified from unligated adapters by spun-column chromatography using sephacryl s-300 and size fractionated on a 1% low melting point mini-gel. Size selected cDNAs (2 - 3 kb) were removed from the gel using agarase (New England Biolabs), phenol:choloroform extracted and precipitated using 0.3 M NaOAC (pH 7)/ethanol. A portion of each cDNA size fraction (0.1 ug) was co-precipitated with 1 ug of lambdaZapII (StratageneEcoRI digested, dephosphorylated arms and then ligated in a volume of 4 ul overnight. Each ligation mix was packaged in vitro using Gigapack II gold packaging extract (Stratagene). We have determined that although first strand cDNA synthesis was initiated using dT, almost all of the cDNAs begin 8-10 bp from the poly-A tail. The reason for the loss of the poly-A tail is most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22313tcn@ibm.cl.msu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   likely due to lower than anticipated nucleotide levels during the Klenow repair of ragged ends before the addition of linkers (3'-5' exo instead of 5'-3' pol). When this library is used please reference the ABRC and: Kieber, J. et al. (1993) Cell 72:427-441.*

a 143 c 133 g 122 t 10 others
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/dev_stage="3 day-old"
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/strain="Columbia"
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                                                                        CCCGAGGTTGATGAAGACCAAGAAGATGGGGATAAAAGATGGGATCCGGATTCAGACATG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gatcagattcgccaacttaagcgcttcaatgttggtgaa 459
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GATGTTGATGATGACCGTAAACCTATACCAAGCAGAGTAAAAAGAGAAGCTGTTGAACCA
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                                                                                                                                                        432;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 457)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4633 World Parkway Circle, St. Tel: 877-577-2733
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Genome Systems, Inc., a wholly owned subsidiary of Incyte
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                                                                                                                                                        Conservative
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Location/Qualifiers
                                                                                                                                                                                                                                                                  /clone_lib="A. thaliana, Ohio State clone set"
/note="cDNA library was made from selected clon
Arabidopsis thaliana Ohio State clone set."
a 132 c 61 g 140 t 23 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP 191
Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li,W.B., Gruber,C., Jessee,J. a
Full-length cDNA libraries and
Unpublished (2001)
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l (bases 1 to 999)
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                                                     /note-Torgan: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library is not normalized, but is the control for the normalized libraries. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA FAX: (1) 301 610 8371 Email:
                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODA011YG11"
                                                                                                                                                                                                                                                               /tissue_type="neuroblastoma cells"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                        /sex="male"
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                 //fulllength.invitrogen.com"
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Query Match Best Local Similarity

22.8%;

Score 412.6; DB 9 Pred. No. 8.9e-94; Mismatches

DB 9;

Length 999;

<u>ب</u>

Gaps

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Conservative

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                                                                                                                                                                                                                                                 tgagatcgitcaatgitcccctactgctcttgggitggitggitggitacactaiccgcaatg 1087
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BG368908
BG368908.1 GI:13258009
EST.
                                              BG368908 775 bp mRNA linear EST 22-OCT-200: HVSME10021D24f Hordeum vulgare 20 DAP spike EST library HVcDNA0010 (20 DAP) Hordeum vulgare cDNA clone HVSME10021D24f, mRNA sequence.
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290 185 230 125

actactatggccaaggtcatcccatgaagccccatcgcatccgcatgacccatgccctcc 289

244

togotoactacggtotocttcagcatatgcaggttotcaagcccttccctgcccgcgaac

ccggacctgatggtgtgaagaggaaagtttgttatttctatgaccctgaggtcggcaatt 229

CCGGCGGACGGCTCGAAGCGCCGCGTCTGCTACTTCTACGACGCGGAGGTGGGCAACT 184

Matches

502;

Conservative

0,

Score 408.6; DB 10; Pred. No. 8.3e-93; 0; Mismatches 135;

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Gaps

DB 10;

Query Match Best Local Similarity

22.6**%**; 78.4**%**;

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Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence start: 9 High quality sequence stop: 706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: rwing@clemson.edu
Total hq bases = 631
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                       http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Als: see Close TJ, Wing R, Kleinhoffs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/gppages/bgn/31/cover.html)* 280 c 216 g 121 t
                                                                                                                                                                                                                                                                                   California, Riverside (Choi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  spikes with awns trimmed were collected at 20 DAP (Fenton ). Total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids in the TJ Close lab at the University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whol
                                                                                                                                                                                                                                                           preparation and sequence analysis see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="20 DAP spike"
/lab_host="SOLR"
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/db_xref="taxon:4513"
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BE053804.2
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                                                                                                                                                                        Clemson University
100 Jordan Hall, Clemson,
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                               Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                      Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simme,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, of the cotton fiber
                                                                                                                           Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 818.
                                                                                                                                                                                                                                        Clemson University Genomics Institute
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                             /organism="Gossypium a:
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA__Ea0035C07f"
/clone_lib="Gossypium arboreum
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KEYWORDS SOURCE

EST

ORGANISM

Homo sapiens Eukaryota; M

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mamumalia; Eutheria; Primates; Catarrhini; Hominidae;

Hominidae;

Euteleostomi;

VERSION

ACCESSION DEFINITION LOCUS

prime, mRNA: AL531607 AL531607.1 (

GI:12795100 sequence

AL531607 AL531607 LTI_NFL001_NBC4

Homo dq sapiens mRNA CDNA

linear Clone C

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EST 13-FEB-2001

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              gaggaaggaacaaacaagg 1612
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                                                        AGTACAAAGTCTGTAGATGTCAGGCCTATGGCTATCGATGAACCAACTGTGAAAGTCGAG
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dpa"
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                                                                      GAGGGTGCTGTACATTGACATTGATATTCACCATGGTGACGGCGTGGAAGAGGCCTTCTA
                                                                                                                                                       TGGCTTCTGTTACGTCAATGATATCGTCTTGGCCATCCTGGAACTGCTAAAGTATCACCA
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Full-length cDNA libraries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corr
South Memorial Parkway Huntsville, AL 35801 For further
call: (800)-533-4363 or contact via email: ccu@resgen.cc
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie-T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann, Butter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann, Watter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann, R., Watter, E., Watter,
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Fax: 314 286 1810
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/note-"Vector: pBluescript II XR; Site_1: EcoR1; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from immature flowers of field grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was XR library construction kit. Complementary DNA was
                                                                                                                                                                                                                                                                                                                                                                  /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1016-6128"
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ctagagctccttaagcagcatgagcgtgttctttatgtcgatattgatatccaccacggg
                                                  CATGCAAAGAAGTGTGAGGCTTCTGGGTTTTGCTATGTTAATGACATTGTGCTGGCTATT
                                                                             cacgctaagaagtgcgaggcctctggcttctgttacgtcaatgatatcgtcttagctatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Shoemaker R/Public
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-*vector: psport! (Life Technologies); Site_1: Not I; Site_2: Sal I; This CDNA library was constructed from mRNA isolated from immature seed coats (200-300 mgs) of greenhouse grown plants. The library was prepared using the Life Technologies psuperScript cDNA library construction kit. Complementary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restriction site. Sal I linker adapters were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I-Sal I restriction site of the psport! vector. The ligated cDNA fragments were transformed into Ecoli ElectroMax DHJDB host cells (Gibco BRL). This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna.*
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78.5%;
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Full-length cDNA libraries and normalization
Unpublished (2001)
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Sequence 7, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. ITILE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 50/080,563 PRIOR APPLICATION NUMBER: 50/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 50/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 50/080,563 PRIOR APPLICATION

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Pred. No. 3e-230;
0; Mismatches 311; Indels 6;
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RESULT US-09-; Seque ; Pate

S-09-282-305-5 Sequence 5, Application Patent No. 6287843

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Best Local Similarity
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
COURRENT FILING DATE: 1999-03-31
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PRIOR FILING DATE: 1998-(
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2
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ORGANISM: Zea
FEATURE:
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Pred. No. 1.2e-216;
0; Mismatches 334;
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 199-03-31
PRIOR APPLICATION NUMBER: 60/80,563
PRIOR APPLICATION NUMBER: 60/80,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (29)...(1405)
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Best Loc
Matches
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LENGTH: 1826
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Pred. No. 2.1e-171;
0; Mismatches 396;
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Matches
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Patent No. 5659016
                                                                                                                                                                                                                                     Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 49008-1699
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP6-227876
FILING DATE: 22-SEPTEMBER-1994
APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DX
SOFTWARE: WORDPERFECT:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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LOCATION: 64.
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CITY: Kalamazoo
                                                                                                                                                                                                 Local Similarity
les 752; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Terryence F. Chapman REGISTRATION NUMBER: 32549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/528,255A FILING DATE: September 14, 1995
                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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Pred. No. 1.8e-151;
0; Mismatches 423;
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MEDIUM TYPE: Diskette,
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DC
SOFTWARE: WordPerfect:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: Furuya Case TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY 1995
ATTORNEY/AGENT IMPORMATION:
NAME: Terryence F. Chapman
                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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CLASSIFICATION: 536
                                                                                                                                                                                                                                                            Local Similarity
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STATE: Michigan
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                                CCGAAAAATGGAAATCTATCGCCCTCACAAAGCCAATGCTGAGGAGATGACCAAGTACCA
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RESULT 6
US-09-282-305-9
; Sequence 9, Application US/09282305
; Patent No. 6287843
; GENERAL INFORMATION:

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LENGTH: 1576
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LOCATION: (38)..(1336)
-09-282-305-9
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APPLICANY: Briggs, Steven P.
APPLICANY: Crane, Virginia C.
TITLE OF INVENTION: Malze Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR FILING DATE: 1998-03-03
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
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Pred. No. 9.9e-142;
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APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases An
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT APPLICATION NUMBER: 60/080,563
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
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; NAME/KEY: CDS
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US-09-282-305-3
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Pred. No. 1.7e-114;
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US-08-998-416-317; Sequence 317, Application US/08998416; Patent No. 6239264
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                               APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                           COUNTRY: US
ZIP: 27709
APPLICATION NUMBER: FILING DATE: 24-DEC
                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtaccatttcaggaaagaccacctgatacagagactcccgaggttgatgaaga 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aaaggtcatgctgagtgcgtcaaatttatgagatcgttcaatgttcccctactgctcttg 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttgcaatgtggtgctgactccctatctggggatcggttaggttgcttcaatctttcaatc
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                                                                                                                                                                                            r: 3054 Cornwallis Road
Research Triangle Park
: No. 6239264th Carolina
                                                                                                                                                                              USA
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Steiner, Sabine
Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Philippsen,
                                                                                                                                                                                                                                                          No. 6239264artis Corporation
  24-DEC-1997
                  US/08/998,416
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                  1099 tggtgctacgagactgg 1115
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                  GGGATACCTATGCTATGTGTCGGTGGTGGAGGTTACACCCCCAGGAATGTGTCGCGGCTA
                                                                                                                                                                                                                                                                                                                                                     GATGAGATCGGATGCTCGCGCGGCAAGCACTTTTCGCTGAATGTGCCGCTCAATGACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGAACGACATTGTTCTGGCGATTCTGAATCTGCTGCGCTACCACCCCACGCGTTCTGTAC
TGGACGTACGAGACAGG
                                                                                                                                    atcgatgatgagagctatcatctgttattcaagcccatcatggggaaagttatggaaatt 918
                                                                                                                                                                                                                              ttccgaccaggggctgtggttattgcaatgtggtgctgactccctatctggggatcggtta
                                                                                                                                                                                                                                                                                                                                                                      caggatataggttatggtagcggaaagtactattctctcaatgtaccactggatgatgga
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                                                                                                 aatgttcccctactgctcttgggtggtggttgcactatccgcaatgttgcccgttgc 1098
                                                                                                                                                                                                           TACAAGCCAACAGTAATTATTCAGCAATGTGGAGCAGACTCTTTGGGGGCATGACAGACTG
                                                                                                                                                                                                                                                                              ATCGATGATGATTCGTACATCAACTTATTTAAGAGCATCATAGACCCGCTAGTTACATCA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCAACTGGTCGGGCGGGCTGCACCACGCCAAGAAGAGCAATCCTTCGGGGTTCTGTTAC
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62.7%;
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RESULT 9
US-08-232-463-14/c
; Sequence 14, Application US/08232463; Patent No. 5670367

GENERAL INFORMATION:

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Query Match
Best Local Similarity
Thes 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)866-3300
TELEFAX: (703)663-4109
TELEX: 899149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                            1310 aggmaagaccacctgatacagagactcccgaggttgatgaagaccaagaagatggggata 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP 91
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29.7
                                                                                                                                                                                                                                                                                                   TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                          1370 aaagatgggatccggattcagacatggatgttgatgatgaccgtaaacctataccaagca 1429
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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1610 agggtgggggggggggggtttcctcctaaaacataagactcggagcttctaatttctt 1669
                                                                         1490 tggagcgtggaaaaggttgtgaggtggaggtggatgagagtggaagcactaaggttacag 1549
                                                                                                                                                                                                                                                           1430 gagtaaaaagagaagctgttgaaccagatacaaaggacaaggatggactgaaaggaatta 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7218 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                              4.7%; Score 85.8; DB 1; ilarity 2.5%; Pred. No. 5.8e-17; Conservative 243; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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26-AUG-1991
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US-08-232-463-14
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                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                  Best Local Similarity 3.3%; Matches 13; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                            1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)886-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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391 ctccgcagcattacccctgaaacccagcaagatcagattcgccaacttaagcgcttcaat 450
                                                                     331 cccttccctgcccgcgaacgtgatctctgccgcttccacgccgacgactatqtctctttt 390
                                                                                                                                           271 egeatgacecatgeeeteetegeteactaeggteteetteageatatgeaggtteteaag 330
                                                                                                                                                                                                               211 gaccetgaggteggeaattactactatggecaaggteateceatgaageeecategeate 270
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OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/232,463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22313-0299
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                                                                                                          Alexandria
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1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                             7218 base pairs
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       RESULT 12
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Best Local :
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CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
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LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.5%; Score 44.6; DB 4; Length 289; llarity 7.5%; Pred. No. 0.00014; Conservative 114; Mismatches 131; Indels
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Sequence 17, Application US/09007005B; Patent No. 625858; GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-07,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEO ID NOS: 33
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APPLICANT: SZOSTAK, Jack W.
APPLICANT: ROBERTS, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
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Best Local Similarity
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TITLE OF INVENTION: SELECTION OF PROTEINS USING FITTLE OF INVENTION: FUSIONS FILE REFERENCE: 00786/350003 CURRENT APPLICATION NUMBER: US/09/007,005B CURRENT FILING DATE: 1998-01-14 EARLIER APPLICATION NUMBER: 60/035,963 EARLIER FILING DATE: 1997-01-27
                                                                                                                                                                                     APPLICANT: Szostak, Jack W. APPLICANT: Roberts, Richard W
                                                                                                                                                                  APPLICANT: Liu, Rihe
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LOCATION: (1)...(289)
OTHER INFORMATION: n =
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TYPE: RNA
ORGANISM: Artificial Sequence
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Pred. No. 0.00014;
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: LCCATION: (1)...(289)
: OTHER INFORMATION: n - A,T,C
US-09-007-005-17
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EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 17
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Matches 19; Conserv
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NAME/KEY: misc_feature
LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C
-09-244-796-17
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APPLICANT: Roberts, Richard W.
APPLICANT: Llu, Richard W.
APPLICANT: Llu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350007
CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
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EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
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                                                                                                                                                                                          LENGTH: 289
TYPE: RNA
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                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                           Query Match
Best Local Similarity
Matches 64; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 8.69
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sakin, Ugur
APPLICANT: Pireundschuh, Michael
TITLE OF INVENTION: Isolated
TITLE OF INVENTION: Thereof
FILE REFERENCE: LUD 5525
                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/177,325B CURRENT FILING DATE: 1998-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                    194 atgtaactgatgagcatggggaaagagggtcttttgctgaaacaga 239
                                                                              317 tgcaggttctcaagcccttccctgcccgcgaacgtgatctctgccgcttccacgccgacg 376
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Search completed: April 28, 2002, 19:24:41 Job time: 8221 sec

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Result
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                                                              830.2
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Copyright (c) 1993 - 2000 Comp
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Novel human polynu	AAF67319	22	399		89.4	45
*	AAS57741	23	286	5.3	96.4	44
Novel human diagno	AAS39024	22	411		97.6	43
Human ovarian canc	AAC89707	22	222	5.5	99.6	42
al cDNA	AAT86374	18	227		105.6	41
breast	AAF17915	22	241	6.7	121.8	40
Human breast cance	AAS47345	22	241	6.7	121.8	39
Fusarium venenatum	AAF07540	21	570	7.3	131.6	38
encoding nov	AAS41223	22	1016		134.6	37
Human polynucleoti	AA161316	22	1539		143	36
CDNA	AAT86373	18	375		150.2	35
al cDNA	AAT86372	18	379	9.2	166.6	34
	AAH55632	22	402		170.4	w w
histone dea	AAZ58261	21	541		186	3 2
	AA159530	22	2046	11.7	211	31
	AAZ93329	21	1654	11.7	211	30
	AAH75178	22	1367	11.7	211	29
	AAH25122	22	1682	11.8		28
hila	ABL01928	23	3826	14.1		27
	AAD17396	22	2009	17.3		26
Drosophila melanog	ABL04120	23	3793	18.3		25
Drosophila melanog	ABL04121	23	1662	21.1		24
Maize histone deac	AAX90838	20	1475	21.3		23
DNA encoding novel	AAS81302	23	1582	23.0	٠	22
hila me	ABL01896	23	4755	23.3	421.4	21
histone	AAC89556	22	1954			20
Maize histone deac	AAX90841	20	1576		9	19
o	ABL01897	23	2145	•	5	18
_	AAT12940	17	2111	•	٠	17
prostate	8	21	2163		•	16
ĕ	AAC89554	22	1611	27.7	499.8	15
encoding	7	18	1449	•		14
nistone dea	AAC89555	22	1985			13
	AAC90323	22	1985	•	504.4	12
METH2 rela	AAZ32066	20	1985		504.4	11
Mouse ischaemic co	ABI99512	24	1997		508.8	10

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ALIGNMENTS

AAF80350

CA2316036-A1. Arabidopsis thaliana. (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA 24-AUG-2000; 2000CA-2316036 27-FEB-2001. Histone deacetylase; AtRPD3A; RPD3; gene expression; transgenic plant; HDA1; ethylene-responsive phenotype; hypocotyl elongation; ds. Nucleotide sequence of a histone deacetylase designated AtRPD3A. 29-JUN-2001 AAF80350; AAF80350 standard; DNA; 1807 (first entry) Location/Qualifiers 142..1647 /*tag= a /product= "histone deacetylase AtRPD3A" ВP

Nucleotide sequenc

Miki B,

Brown D,

Tian L,

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CC The present sequence encodes an Arabidopsis thaliana histone deacetylase designated AtRPD3A. The protein is homologous to yeast RPD3 and HDA1. CC The polynucleotide sequence is used in the method of the invention. CC The specification describes a method for regulating gene expression in CC transgenic plants. The method comprises modifying histones by introducing CC chimeric nucleotide sequences which have regulatory elements in operative association with a gene of interest or with a nucleotide sequence encoding histone deacetylase. The method is useful for regulating the developmental, physiological or biochemical pathway within a plant, CC particularly for repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation). The method is also useful as a functional test for identifying a phenotype associated with perturbing a gene. The histone deacetylase genes are useful for altering the development of an organism.
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Best Local
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                                       cacggcctctgcgatattgccatcaactgggctggtggtctccatcacgctaagaagtgc
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Best Local Similarity
Matches 1021; Conserv
                                                                                                                                                                                                                                     The present sequence is that of cDNA clone srl.pk0023.dl encoding soybean histone deacetylase 1 (HDI, see ANY58829), a chromatin associated protein. The cDNA clone was isolated from a soybean root cDNA library on the basis of homology to other plant histone deacetylases. The invention relates to isolated rice, soybean and wheat nucleic acid fragments encoding HDI. It also relates to the construction of a chimeric gene encoding all or a portion of HDI, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of HDI in a transformed host cell. The availability of nucleic acid sequences encoding (portions) of histone deacetylase proteins will facilitate studies of global transcriptional regulation in eukaryotic cells,
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                                                      altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maize histone deacetylase; family 1, ZmHD1; promoter regulator; promoter; RNA polymerase II; transcription; plant transformation; heterochromatin; disease resistance; chromatin assembly; gene activity; toxin screening;
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                                                                                                                                                                   belongs to family 1, ZmHD1 and appears to be regulator of promoters fo RNA polymerase II, for transcription of genes. The nucleotide sequence can be used to transform plants and increase disease resistance by
                                                                                                                                                                                                                                                                                                                Claim 1;
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The present sequence is that of a contig encoding a portion (see AAY58828) of rice histone deacetylase 1 (HD1), a chromatin associated protein. The contig was obtained from cDNA clones (solated from rice callus, 15-day-old leaf and 15-day-old seedling cDNA libraries on the basis of homology to other plant histone deacetylases. The invention relates to isolated rice, soybean and wheat nucleic acid fragments encoding HD1. It also relates to the construction of a chimeric gene encoding all or a portion of HD1, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of HD1 in a cross-corned host cell. The availability of nucleic acid sequences encoding (portions) of histone deacetylase proteins will facilitate studies of global transcriptional regulation in eukaryotic cells,
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                     RNA polymerase II, for transcription of genes. The nucleotide sequence can be used to transform plants and increase disease resistance by altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find the in screening for toxins that affect pathogenicity and in determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1198
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                                                                                                                         Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize histone deacetylase; family 1, ZmHD1; promoter regulator; promoter RNA polymerase II; transcription; plant transformation; heterochromatin; disease resistance; chromatin assembly; gene activity; toxin screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1242
                                                                         altering the levels of heterochromatin, altering chromatin assembly, and gene activity of the transformed plants. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining
                                                                                                                                                            The present sequence encodes a maize histone deacetylase. This DNA belongs to family 1, ZmHDl and appears to be regulator of promoters for belongs to family 1, Tor transcription of genes. The nucleotide sequence RNA polymerase II, for transcription of genes. The nucleotide sequence can be used to transform plants and increase disease resistance by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1192
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                                                   disease response promoters are regulated by histone deacetylase.
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-01	AUG-19	PR	25-MAY-1999;
01.0	02-AUG-1999; 02-AUG-1999;	קר א א	24-MAY-1999;
9	2-AUG-19	P P	20-MAY-1999;
-01,		יים א	
01.		PR	14-MAY-1999;
-01,	27-JUL-1999;	PR	14-MAY-1999;
91		מק	14 - MAY - 1999;
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-01,	19	PR	07-MAY-1999;
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2 2	- 5	PR	05-MAY-1999;
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-014	19	PR	1999;
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-014	5	PR	00-364-2000
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201	23-JUN-1999;	ק ק	ation assay; genetic ma
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919	نز نز	PR	1300 gtaccatttcaggaaagaccacctgatacagagactcccgaggttgatgaaga
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99US-0139119	14-JUN-1999;	PR	1240 cttgaagagattegeaatgacetteteeacaatetetetaagetteageatgeteeaagt 1299
2 2	10-JUN-1999;	יים א א	1082 cctgattatactcttcatatccaaccaaaagtgttgaaaacctgaataccacaaaggac 1141
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                                                                                                                                                                                                                                                  The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI99212, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition improving drugs or therapeutics for ischaemic diseases. ABI99913 and ABI9914 represent PCR primers for a mouse ischaemic condition related sequence, the condition related sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
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                        ccctcctcgctcactacggtctccttcagcatatgcaggttctcaagcccttccctgccc
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                                                                                                                                                                              respectively. METH1 and METH2 have been found to be potent inhibitors of cancer and other disorders related to angiogenesis both in vitro and in vivo. They can be used for treating ceancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis, AAZ32080, and AAY49503 to
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Best Local
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cancer; diagnosis; hyperproliferative disorder; autoimmune disease;
anglogenesis inhibitor; abnormal wound healing; inflammation;
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                                                                                                                                                                                                                AAY49511 represent sequences given in the exemplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
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22-DEC-1999;
22-FEB-2000;
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20-JUL-1999;
10-AUG-1999;
                   The present invention relates to human METH1 and METH2, (ME for metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003). The present sequence is an expressed sequence tag (EST) for METH. METH can be used for inhibiting angiogenesis in an individual, and for treating cancer, benigh tumours, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler-Webber syndrome, plaque
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                                                                          The present invention provides inhibitors of histone deacetylase enzymes such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These inhibitors may be antisense strands or they may be compounds identified by contacting the enzyme with the compound and measuring the resulting enzyme activity. These inhibitors are useful for treating cancers and for identifying which histone deacetylase is involved in a neoplasia.
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           The present cDNA sequence encodes a novel histone deacetylase (HDX)
CD polypeptide, designated HD1. The HDX polypeptides are capable of modulating proliferation survival and differentiation of cells. The modulating proliferation survival and differentiation of cells. The proteins are able to alter chromatin structure by deacetylating histones consists are able to alter chromatin structure by deacetylating histones consisted as H3 or H4. They have the ability to modulate cell growth by confidencing cell cycle progression or to modulate gene transcription. The products can be used for diagnosis and therapy. They can be used, for cells consisted to treat tumours or proliferative disorders or spermatogenesis, consteogenesis, chondrogenesis or the differentiation of progenitor cells. They can also be used to treat psoriasis, bone diseases, for they can also be used to treat psoriasis, bone diseases, consistency increasing bone density, liver repair subsequent to a partial hepatectomy, to promote regeneration of lung tissue in the treatment of the cartilage, increasing bone density, liver repair subsequent to a partial conspilant recipients. HDx inhibitors can be used as anti-fungal agents, preservatives in foodstuff, feed supplements for promoting weight gain in coll subtract in defoliants. The products can be used in coll subtract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Histone deacetylase gene; HDx; HDl; HDx polypeptide; deacetylation; H3 H4; cell differentiation; chromatin structure; cell cycle progression; prolliferative disorder; fibroprolliferative disorder;
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                                                                                                                                                                                                                                                                                                                                                                                     New isolated histone deacetylase polypeptide(s) and genes -develop products for modulating the proliferation, survival differentiation of cells, e.g. for treating tumours.
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                                                                                                                                                                                                                The present invention provides inhibitors of histone deacetylase enzymes such as HDAC-1, HDAC-2, HDAC-3, HDAC-4, HDAC-5, HDAC-C and HDAC-D. These inhibitors may be antisense stands or they may be compounds identified by contacting the enzyme with the compound and measuring the resulting enzyme activity. These inhibitors are useful for treating cancers and identifying which histone deacetylase is involved in a neoplasia.
                                                                                                                                                                                                                                                                                                                                                      Antisense oligonucleotide that inhibits expression of a histone deacetylase, useful for treating and/or alleviating the symptoms neoplasia, or for inhibiting neoplastic cell growth in an animal
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ALIGNMENTS

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	wn, D.C.	Wu, K., Miki, B.L., Tian, L. and Brown, D.C.	:i,B.L., T	Wu, K., Mik	AUTHORS
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Direct Submission
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Agriculture and Agri-Food Canada, Ot
Location/Qualifiers
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 ctttattccttttgccagacctatgctggaggatctgttggtggctctgtcaagcttaac
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/protein_id="AAC28474_1"
/db_xref="GI:11066139"
/fbrotein_id="MAC28474_1"
/db_xref="GI:11066139"
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VNDIVLAIEBLLKQHERVLYVDIDIHHGDGVEEAFYATDRYMTVSFHKFGDYFPGTGH
IQDIGYGSGKYYSLAVPLDDGIDDESYHLLFKPIMKYWEIFRRGAVVLQCGADSILG
IQDIGYGSGKYYSLAVPLDDGIDESYHLLFKPIMKYWEIFRRGAVVLQCGADSILG
DRLGCFNLSIKGHAECYKFMRSFNVPFLLLLGGGGYTIRNVARCWCYETGVALGVEVED
KMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEIRNDLHNLSKLQHAPSVPFQER
PPDTTETPEVDEDGDGDKWHDDSDMDYDDDRKPIPSRVKREAVEPDTKDKDGLKGIM
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                                                Submitted (26-FEB-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.biochem.mpg.de.mayer@mips.biochem.mpg.de.project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
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Direct Submission
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Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosome 4 can
viewed at: http://websvr.mips.biochem.mpg.de/proj/thal/.
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LAQPDFVTSTRFSHLEIPTHTIWLGACNHALPEDVFAKRIKSLLSLSVODLTLNLGLV
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/PROCESSI-AGE
/P
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12071...12191,12300...12463))
/gene="F20D10.20"
/note="similarity to Caenorhabditis
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//gene="F20D10.20"
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complement(join(830..2566,2624..3049))
/gene-"F20D10.10"
/note-"strong similarity to retrotransposon -like
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830. .3049
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/gene="F20D10.10"
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YSGAERMLTSARALLVQYGLSSSDSCLRGLEAELADLNRLRGRHVAVKSPEPVVQKSE
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                                                                                                                                                                                                                                                                                                                                                                              contains EST gb:N97112;AA728688*
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/chromosome~"4"
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                                                                                                                                                                                                                                                         /translation="masysafksysangknsmpgklgylapppgspydndvigidld
trinscvsymegktarvienaegsrtfsyvamngkgellugfdekrqavinpyntigidlg
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skrligreddpotogkerkmypykivkamngbergspsgidanultkygmnnk
egviavedpatydayfndagroatkdagkiagldvor iineptaaalsygmnnk
egviavedpatydayfeldagroatkdagkiagldvor iineptaaalsygmnnk
egviavedpatydsileissgverkkatnodtelogedpuntlleylynefkrsb
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sovetstaadhomovgikvlogeremaadnevlegeblvgippapkgmpietevetpida
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schttivsakdkatgkeonitiessgglsddeinkykeaelnaokdogerkollidlrus
kgittvsakdkatgkeonitiessgglsddeinkykeaelnaokdogerkollidkak
sovetstaadhoksterensovenseterakese
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PPTRSETVLHLYQARPSLKGSCFLPMLRKVRLAKSFTRVDCETETEV INLOMRISNDA
APKGDRRQVIGVKECGETYVLAEYDGTFWSLLDSKWSLKQTCNPATDGPLFELSGTRM
VKVYSGRKLEYEPKHCSLLRSEQDFMTAVEFSKQHPYCRAVGLLDLKFGSIEANEKWL
VLPGMYSSFILSDLLKKEGFSAAAKDTYKANGITEESTEIDVLSQEKLEEETMMDVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F20D10.30"
complement()oin(13386. .14030,14118. .14738,1482
15491. .15569,15669. .15730,16043. .16069))
/gene="F20D10.30"
/note="strong similarity to dnaK-type molecular
PHSP1 -Pisum sativum, PID:g20835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contains ATP/GTP-binding site motif A (P-loop) [AEAYLGKS] Heat shock hsp70 proteins family signatures [IDLGTTNS], Hsp70_2 [VPDLGGGTFVVSIL], Hsp70_3 [VLLVGGMTRVFKVQE] contains EST gb:T44452, Z24523, T04782, Z17893, Z17973*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(13386. .14030,14118. .14738,14828. .15394,
15491. .15569,15669. .15730,16043. .16069))
/gene-*F20D10.30*
13386. .16069
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/gene="F20D10.20"
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/gene="F20D10.20"
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/gene="F20D10.20"
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complement(14739.
/gene="F20D10.30"
/number=2
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                                                                              /gene-"F20D10.30"
                                                                                                                                                               complement(14031.
                                                                                                                                                                                                                         complement(13386.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                  gaagececategeateegeatgacecatgeeeteetegeteaetaeggteteetteagea 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agtttgttatttctatgaccctgaggtcggcaattactactatggccaaggtcatcccat 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        agaggtaatggatactggcggcaattcgctggcgtccggacctgatggtgtgaagaggaa 194
                                                                tattgccatcaactgggctggttgttccatcacgctaagaagtgcgaggcctctggctt 614
                                                                                                                                                                                                       CCAGACCTATGCTGGAGGATCTGTTGGTGGCTCTGTCAAGCTTAACCACGGCCTCTGCGA
                                                                                                                                                                                                                         ccaqacctatgctggaggatctgttggttggctctgtcaagcttaaccacggcctctgcga
                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAGGTAATGGATACTGGCGGCAATTCGCTGGCGTCCGGACCTGATGGTGTGAAGAGGAA 87023
                                           CTGTTACGTCAATGATATCGTCTTAGCTATCCTAGAGCTCCTTAAGCAGCATGAGGTTTG
                                                                                                                          TATTGCCATCAACTGGGCTGGTGGTCTCCATCACGCTAAGAAGTGCGAGGCCTCTGGCTT
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complement(16556.
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complement()oin(16556. .16790,16869. .17056,17133. .17377,
17453. .17618,17710. .17975,18152. .18358,18789. .19503))
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/number=5
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/gene-*F20D10.30*
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/gene="F20D10.30"
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/gene="F20D10.30"
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Pred. No. 1.1e-258;
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	REF		SOU	VER	LOCUS	RESULT	Дb	Qy	Db	δ 8	3 2	DЬ	Qy	DЬ	Qy	B ₀	Qy	D	Qy	Dβ	Qy	B	Qy	₽	Qy	Дb	Qy	ф	γο.	B 5	2 5	} Q	Db
	REFERENCE		SOURCE ORGANISM		TOTON	RESULT 5 ATCHRIV89/c	85702 TA	1301 ta		1241	1181 08	85882 CI		85942 TO	1109	86002 TA	1109	86062 TJ	1071 tt	86122 To	1011 tg	86182 To	951 tç	86242 GC	891 gc	86302 TT	831 tt	86362 TO			711 30	668	86542 то
	Rosidae	Eukaryo Spermat	thale cress Arabidopsis	AL161593 AL161593.2	ATCHRIV		ACCATTTO	accattto	rgaagaga	tgaagaga	agactata	ACTTGGAG	acttggag 	BACGCCTC		ATGCTGCT		TACACTAT	Lacactat	AGTGCGT	gagtgcgt	CTGATTO	gctgacto	CCATCAT	ccatcat	CTCTCAA	ctctcaa	SATTACTI	gattactt 	TGGAGGA	וונכוכוכו		CACCTGC
	es 1623	~ <		3.2 GI:7	789 789		AGGAAAG	:aggaaag	TTCGCAA	ittogoaa	cacttca	TTGAAGT	ttgaagt	TCTTTCT	1	CTAGCTT	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CCGCAAT	ccgcaat	CAAATTT	caaattt	ATTGTCT	cctatct	GGGGAAA	ggggaaa	TGTACCA	tgtacca	TCCCGGT.	teeeggt	GGCATTT	7773+++		ACCGTTT
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	assicacea	m.		t, concre)) †		AGGT 8566	aggt 1343 	AGCTTCA	lagettead	lataagaa.	AATATTA		TTATATG	1	TGTACCA		GGTACTT		ACTECTO	actgete	TCTTTCA	itetttea:	GGCTGTG	ggctgtg	GAGCTAT	gagctat	TTATGGT	ttatggti	TGTCTCG	TGATATO	tgatato	GTCGTTT
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Towart	/number=3	complement (6170. /gene="AT4g38130"	complement(6112. /gene="AT4g38130" /number=3	complement(5684. /gene="AT4g38130" /number=2	number=2	/number=1 complement(5612.	complement (5538. /gene="AT4g38130"	KMYCHEXYXXYYGDDYTHVAYSNMEINNSKOMLEEIRNULLHILSKLOHAPSVPYOOR PPDTETPEVDEDQEDGDKRMDPDSDMDVDDDDRKPIPSRVKKEAVEPDTKDKDGLKGIM EROKGCEVDYDESGGTKVTGVNDVGVEFEASVKMEEEGTNKGGARGAFDXK"	IQD I GYGSGKYYSLRIVPLDG I DDESWHLLFK FLIMKKWAEI FRRGAVILLOGGADSISSON I DDESWHLLOGGADSISSON I DDESWHLLFK FLIMKKWAEI FRRGAVILLOGGADSISSON I DDESWHLLOGGADSISSON I DDESWHLOGGADSISSON I DDESWHLOGGADS	NYGEDCPVEDGLYSFCQTYAGGSVGGSVKLHADDYAVSTLKSTTFETQODQLTQLKKF NVGEDCPVEDGLYSFCQTYAGGSVGGSVKLHAGLCDIAINWAGGLHKAKKCEASGFCY VNIJVLAILELLKOHERVLYVDIDIHHADGVERAFYATDRWMYSFHKAKKCEASGFCY	db_xxef="G1:7270797" 'db_xxef="G1:7270797" 'translation="MDTGGNSLASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIR	/product="Histone deacetylase" /protein id="CARR0478.1"	AW004334.1, F15302, AA605428* /codon start=1	e="AT4g	/yene= AiryJ0130 complement(join(54335537,5 62586328,65846814,6945.	Complement()01n(5433553/,56125683,61126169 62586328,65846814,69457385,74707997)) //dono="ATA/18130"	/gene="AT4g38130"	er:	/cnromosome="4" complement(5433.	ref="taxon:3702"	organism="Arabidopsis	ation/Qua	has an	n perfor	ohn Inne el.bevar	Mike Bev	Klopfer	sion		Kutzner,M.,	Mayer,	195922 to 1 , Braeken, M.	Ridley,P., Hudson,S., Mewes,H.W., Lemcke,K.
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agaggtaatggatactggcggcaattcgctggcgtccggacctgatggtgtgaagaggaa 194
                                                                                                               AGAGGTAATGGATACTGGCGGCAATTCGCTGGCGTCCGGACCTGATGGTGTGAAGAGGAA
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GTRLPNGEAYPSEEARETANATNHPGGEKERT1LELTAELERTGQRCEVYRANLLS1L
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FDSLEVKANCSCQMFEYSGIICRHILAVFSAKNVLALPSRYLLRRWTKEAKIRGTEEQ
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38. .1591
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Sequence 7 from par168366
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Baldwin, D.Adelphi., Briggs, S.P. and Cran
Maize histone deacetylases and their use
Patent: US 6287843-A 7 11-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.
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Pred. No. 2e-197;
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AF332875
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1 (bases 1 to 1579)
                                                                                                                                                     Song, F. and Goodman, R.M.
Direct Submission
Submitted (30-DEC-2000) Department of Plant Pathology, University of Wisconsin-Madison, 1630 Linden Drive, Madison, WI 5706, USA
                                                                                                                                                                                                                                                                                                                                                          Oryza
                                                                                                                                                                                                                                 Unpublished
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/codon_start=1
/product="histone deacetylase
/protein_id="AAK01712.1"
                                                 /dev_stage="seedling"
13. .1494
                                                                             /cultivar-"Yuanfengzao"
/db_xref-"taxon:4530"
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                                             CATCTTCAAGCCGATCATCAGCAAAGTCATGGAGAGTGTATCGTCCTGGTGCAGTCGTGCT
                                                                                                                               GAAGTATTACTGCCTGAATGTCCCGCTGGATGATGGGATTGATGATGACAGCTACCAGTC
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SLSGDBRIGCFNLSGKGHAECVKFMRSFNVPLLLLGGGCYAIRNVARCWCYETGVALGH
ELTDKMPPNEYFEYFGPEYSLFVAASNMENRNTNQLEIKCNILDNLSKLQHAPSVQ
FEERIPETKLPEPDEDQEDPDERHDPDSDNVLDDHKPMGHSARSLIRNIEVKREITES
EAKDQHGKRLTTEHKGPEPMADDPGSSKQAPVSRRLLYPSANP*

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PHRIRMTHALLAHYGLLDQMQVLKPHPARDRDLCRFHADDYVAFLRSVTPETQQDQIR
ALKRPNYGEDCDVFDGLYSFCOTYAGGSVGGAVKLNHGHDIAINWAGGLHHAKKCEAS
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Zea mays put
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification and characterisation of an RPD3 homologue from (2ea mays L.) that is able to complement an rpd3 null mutant c Saccharomyces cerevisiae
Mol. Gen. Genet. 258 (3), 288-296 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rossi, V., Hartings, H. and Motto, M.
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                  /product-"putative histone deacetylase RPD3"
/protein_id-"AAC50038.1"
/protein_id-"AAC50038.1"
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            ttgcttcaatctttcaatcaaaggtcatgctgagtgcgtcaaatttatgagatcgttcaa
                                                CCGCCTGGTGCAGTTGTGCTTCAGTGTGCTGATTCCTTGTCTGGGGATAGGTTGGG
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REFERENCE
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SOURCE
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1 (bases 1 to 2019)
Baldwin, D.Adelphi., Briggs, S.P. and Crane, V.C. Maize histone deacetylases and their use Patent: US 6287843-A 5 11-SEP-2001;
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patent US 6287843
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Pred. No. 1.3e-185;
0; Mismatches 334;
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RESULT 12
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LOCUS
DEFINITION
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                                     GACTGCCCCGTGTTCGACGGTCTCTTCCCCTTCTGCCAGGCCTCCGCTGGGGGAAGCATC
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1 (bases 1 to 1742)
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OFHDRRSDPEAPEEKEEDMDKRPPQRSRLMSGGAYDSDTEDPDSLKSEGKDVTANFQM
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/cultivar="Cuzco"
/db_xref="taxon:4577"
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/db_xref="GI:4193320"
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Sequence 1 from patent US 6287843.
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Baldwin, D. Adelphi., Briggs, S.P. and Crane, V.
Maize histone deacetylases and their use
Patent: US 6287843-A 1 11-SEP-2001;
Location/Qualifiers
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Sidorenko, L., Selinger, D., Kaeppler, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chandler, V.L., Kaeppler, S.M., Kaeppler, H.F. and Cone, K.C. Sequences from the Plant Chromatin Consortium (NSF Plant project 9975930)
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/protein_id="AAL33653.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J., Chan,M. M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C.J., Shinn,P., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-JAN-2002) Plant Gene Expression Center, 800 Buchan Street, Albany, CA 94710, USA RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki.M., Narusaka,M., Ishida,J., Satou.M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Pamada, K., Banh, J., Chan, M.M., Onodera, C.S., Quach, H.L., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AY072201
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                                                                                                                                                                                                                                                                                                                                         ctqyaggatctqttggtggctctgtcaagcttaaccacggcctctgcgatattgccatca
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1492. .1704
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363 c 433 g 454 t
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66.0%;
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Pred. No. 1.2e-136;
0; Mismatches 395; Indels
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ORIGIN

Search completed: April Job time: 9248 sec 28, 19:26:38

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                     Database :
                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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2722
1 MDTGGNSLASGPDO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MDTGGNSLASGPDGVKRKVC.....KMEEEGTNKGGAEQAFPPKT 501
                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                      sp_organelle:*
sp_phage:*
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1646.426 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	-	14	13	12	11	_	9	8 1	7]	6	5	4	w	N	_	No.
1298	1307	1313	1320.5	1329.5	1334	1336	1358	1359	1361.5	1374	1496.5	1496.5	1548	1561.5	1568.5	1958.5	2134.5	2719	Score
47.7	48.0	48.2	48.5	48.8	49.0	49.1	49.9	49.9	50.0	50.5	55.0	55.0	56.9	57.4	57.6	72.0	78.4	99.9	Query Match Length
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Q9mln6 arabidopsis	Q9xyc7 plasmodium	Q9vnc2 drosophila	Oguae cryptospori	Q9clc6 cochliobolu	062339 caenorhabdi	059702 schizosacch	Q9jlx5 mus musculu	Q9jm08 mus musculu	Q9p4f5 emericella	Q99pa0 rattus norv	Q9vzal drosophila	077213 drosophila	Q9ztp8 zea mays (m	Q9fve5 arabidopsis	Q9fml2 arabidopsis	Q9axf0 oryza sativ	Q91kg1 mesembryant	Q9szl3 arabidopsis	Description

Query Match Best Local Similarity

> 99.9**%**; 99.8**%**;

Score 2719; DB 10; Pred. No. 5.3e-205;

Length 501;

33 389.5 34 389.5 35 367.5 36 37.5 37 317.5 38 309.5 40 299.5 41 298.5 42 296.5 44 296.5 45 296.5	20 1259 21 1240 22 1198 23 1138 24 1006 25 885 26 887 27 847 28 759.5 29 644.5 30 594.5
	446.3 77337.08 1177.3 10.3 10.3 10.3 10.3 10.3 10.3 10.3 10
36/ 158 883 380 1108 425 142 1215 1310 310 310 310 310 310 310	566 4409 4481 377 377 377 377 377 377 377
2 Q99X04 2 Q99TC9 10 Q9LXNB 5 Q9XX1 2 Q9HXMI 1 Q9FNQ7 10 Q9FNQ7 10 Q9M1NB 4 Q94975 4 Q94586 4 Q94583 10 Q9LS38	3 Q9HDT2 5 Q9GU59 5 Q9FHQ9 Q9FHQ9 1 Q9FHQ4 4 Q9HP76 4 Q9NP76 4 Q9NP4 11 Q9D0K6 5 Q9GRP1 11 Q9DA2 11 Q9PA2 11 Q9PA2 2 Q9FXX1
Q9wx04 streptomyce Q9ptc9 staphylococ Q9lxn8 arabidopsis Q9xx1 drosophila Q9hxm1 pseudomonas Q9fnq7 arabidopsis Q9sje6 arabidopsis Q9m1n8 arabidopsis Q9m1n8 arabidopsis Q9m1n8 arabidopsis Q9d975 homo sapien Q67877 aquifex aeo Q9nzs3 homo sapien Q9ls38 arabidopsis	O9hdt2 ustilago ma O9gu59 cryptospori O9fh09 arabidopsis O9gt74 tetrahymena O9pt76 homo sapien O9nyh4 homo sapien O9nyh4 homo sapien O9d0k6 mus musculu O9grp1 leishmania O9pyb2 rattus norv O9h368 homo sapien O67135 aquifex aeo O9k7x1 bacillus ha

ALIGNMENTS

SO DR	R R R R R	R R R R R	R R R R R	R R R R R R R	8888B	RESULT Q9SZL3 ID Q AC Q DT 0 DT 0
EMBL; ALIO3336; CABS0783; EMBL; ALIO3336; CABS0788; InterPro; IPR000288; His_deacetylse. Pfam; PF00850; Hist_deacetyl; 1. PRINTS; PR01270; HDASUPER. SEQUENCE 501 AA; 56023 MW; 857D2E3D16B7CC1F CRC64;	Η.	SEQUENCE FROM N.A. SEQUENCE FROM N.A. Wedler H., Kutzner M., Wambutt R., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	(FEB 1999) to the EMBL/GenBank/DDBJ databases. [2] SEQUENCE FROM N.A. EU Arabidopsis sequencing project; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.	ID-3702; FROM N.A. , Wedler H., Kutzner M., Wambutt R., 1 F.X., Schueller C.; d (FEB-1999) to the FMRI/GenRank/DDRI	CETYLASE. OR AT4G38130. Ithaliana (Mouse-ear or Viridiplantae; Streptota; Brassicales; Brassic	ILT 1 (1) (1) (1) (2) (2) (3) (3) (4) (5) (5) (5) (5) (7) (6) (7) (7) (7) (7) (7) (7) (7) (7) (7) (7

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SEQUENCE
                                                                                                                                                                                         Submitted (JUN-2000) to the EMBL/GenBank/DDBJ
EMBL; AF282888; AAF82385.1; -
InterPro; IPR000286; H1s_deacety1se.
Pfam; PF00850; H1st_deacety1; 1.
PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                         Scharte J., Baur B.; 
"Molecular cloning of histone deacetylase 
crystallinum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mesembryanthemum crystallinum (Common ice plant).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Alzoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                          TISSUE-LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-3544;
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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79.8%;
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                                                                ; Score 2134.5; DB 1; Pred. No. 3.5e-159; 31; Mismatches 61;
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Best Local
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01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                 EMBL; AF3
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (Rice).
Eukaryota; Viridiplantae;
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
HISTONE DEACETYLASE HD1.
                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-2000) to the EMBL/GenBank/DDBJ EMBL; AF332875; AAK01712.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                OsHD1."
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Song F., Goodman R.M.;
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Ehrhartoideae: Oryzeae; Oryza;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9AXF0
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                                                                KPFPARERDLCRFHADDYVSFLRSITPETQODQIRQLKRFNVGEDCPVFDGLYSFCQTYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                        of a rice histone deacetylase
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Last annotation updat
                                                                                                                                                                                                                                                              Score 1958.5;
Pred. No. 2.26
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DNA res. 4:401-414(1997).
EMBL: ABOOB255; BAB10553.1;
InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASOPER.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Nakamura Y., Sato S., Kaneko T.,
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YIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDG
                             YVDIDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDG
                                                                                                                                                                  TYAGGSYGGSYKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIYLAILELLKQHERYL 179
                                                                                                                                                                                                                              SRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCR 123
                                                                                                                                                                                                                                                                                LKPFPARERDLCRFHADDYVSFLRSITPETQQD--QIRQLKRFNVGEDCPVFDGLYSFCQ 119
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                                                                                                                                                                                                                                                                                                                                                                            DTGGNSLASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQV
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60.9%;
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Wu K., Malik K., Tian L., Brown D., Miki B.;
"Functional analysis of RPD3 histone deacetylase
Arabidopsis thaliana.";
Submitted (oCT-1999) to the EMBL/GenBank/DDBJ da'
EMBL, AF195548; AAG28475.1; -.
InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
SEQUENCE 471 AA; 52720 MW; 371BF7040E508849
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O9FVE5;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                         ASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVL
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MDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSY
                                                                                                                                                     TYAGGSVGGSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVL
                                                                                                                                                                                    {\tt SRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCR}
                                                                                                                                                                                                                                                    DESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATYESDSDDDDDKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --DSDMDVDDDRKPIPSRVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTKVTGVN 472
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                                                                                                                                                                                                                                                                                                                               57.48;
                                                                                                                                                                                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                               Score 1561.5;
Pred. No. 2.86
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                                                                                                                                                                                                                                                                                                                  Mismatches
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deacetylase homologs
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01-MAY-1999
01-JUN-2001
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Pipal A., Wegener S.;
Pipal A. (JAN-1998) to the EMBL/GenBank/DDBJ
EMBL; AF045473; AAD10139.1;
Mendel; 39025; Zeama; 3043;39025.
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Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
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                                                                                   GGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQM
                                                                                                                                                                                         LLFKPIMGKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLL
                                                                                                                                                                                                                                                                                             HCDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYH
                                                                                                                                                                                                                                                                                                                                                                                                   GGSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIH 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLFQCIIKKVMEVYQPDVVVLQCGADSLAGDRLGCFNLSVKGHADCLRFLRSYNVPMMVL
                                                                                                                                                                                                                                                                                                                                                                        GAAVKLNRGDADITVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKFHRRVLYVDIDVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARERDLCRFHADDYVSFLRSITPETQODQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSV 126
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                                                        GGGGYT I RNVARCWCYETAVAVGVEPDNKLPYNDYYEYFGPDYTLH I QPKSVENLNTTKD
                                                                                                                                                                                                                                                                    HGDGVEEAFFTTNRVMTVSFHKYGDFFPGTGHITDVGAAEGKHYALNVPLSDGIDDTTFR
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(TrEMBLrel. 10,
(TrEMBLrel. 17,
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63.3%;
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Last sequence up
Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Best Local Similarity
Matches 268; Conser
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01-NOV-1998 (TrEMBLrel. 08, La
01-JUN-2001 (TrEMBLrel. 17, La
PUTATIVE HISTONE DEACETYLASE.
RPD3 OR CG7471.
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077213;
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
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                                                                                                                           VARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEEIRNDLL
                                                                                                                                                                                                                                          YATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMGK
                                                                                                                                                                                                                                                                                                  LCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAF 195
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                                                     ENLRMLPHAPGYQIQAIPEDAINDESDDEDKYDKDDRLPQSDKDKRIVPENEYSDSEDEG
                                                                               HNLSKLQHAPSVPFQERPPDTETPEVDED-----
                                                                                                             VSRCWTYETSVALAVEIANELPYNDYFEYFGPDFKLHISPSNMTNQNTSEYLEKIKNRLF
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EGGRRDNRSYKGQRKRPRLDKDTNSNKASSETSSEIKDEKEKGDGADGEESTASNT
                                                                                                                                                                                                                           YTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNIPLRDGMDDDAYESIFVPIISK
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                       -DRKPIPSRVKREAVEPDTKDKDG-----LKGIMERGKGCEVEVDESGST 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1496.5; DB Pred. No. 4e-109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                 -QEDGDKRWDPDSD-MDVDD--
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481
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RA Beesson K.Y. Benos P.V. Berman B.P. Brokardi D. Beasley E.M.,
RA Beesson K.Y. Benos P.V. Berman B.P. Brokardi D. Bolshakov S.
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortis K.C. Busam D.A. Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C. Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dietz S.M.,
RA Dodson K.J. Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., House M., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McPherson D.,
RA Meison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spiar E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhan M., Zhan G., Zhao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Shong W., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Smith H.O.,
RA Zheng S.H., Wers E.W., Rubin G.M., Venter J.C.;
RT Teperoc JER0015805; Ryd3.
DR Filybase; FBgn0015805; Ryd3.

DR Filybase; FBgn0015805; Ryd3.
                                                                                                                                                                                                                                           Query Match
Best Local :
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
Wan I.F., Agbayani A., An H.-J., Andrews-Ffannkor C., Baldwin D.,
The Company of the Company o
                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00850; Hist_deacetyl;
PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9VZA1
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                         HADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHG 135
                                                                                                                    KRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFFPARERDLCRF
                                                                                    KKRYCYYYDSDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKATADEMTKF
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000286; His_deacetylse.
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                                                                                                                                                                                                               Conservative
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56.3%;
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80;
                                                                                                                                                                                                                                           Pred.
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Best Local
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Q99PA0; PRELIMINARY:
Q99PA0;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                              Wilquet V., Chavez M., Korbers R., Geerts A.;
"Expression pattern of rat histone deacetylases.";
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF321131; AAKI1184.1; -.
SEQUENCE 428 AA; 48829 MW; 7CB448CFE33041FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-WISTAR; TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
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                                                                    183
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                                                                                                                                                 CDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAFY
VVDFYQPXCIVLQCGADSLGCDRLGCFNLSIRGHGECVEYVKSFNIPLLVLCGGGYTVRN
                                                                 LTDRVMTVSFHKYGNYFFPGTGDMYEVGAESGRYYCLNVPLRDGIDDQSYKHLFQPVISQ
                                                                                   ATDRVMTVSFHKFGDY-FPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMGK
                                                                                                                                CDIAINWAGGLHHAKKFEASGFCYVNDIVIGILELLKYHPRVLYIDIDIHHGDGVQEAFY
                                                                                                                                                                                               SEDYIDFLQRVSPTNMQGFTKSLNAFNVGDDCPVFPGLFEFCSRYTGASLQGATQLNNKI 122
                                                                                                                                                                                                                                ADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHGL 136
                                                                                                                                                                                                                                                              KTVAYFYDPDVGNFHYGAGHPMKPHRLALTHSLVLHYGLYKKMIVFKPYQASQHDMCRFH 62
                                                                                                                                                                                                                                                                                               RKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRFH
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                                VMEIFRPGAVVLOCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTIRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DRKPIPSRVKREAVEPDTKDKDG------LKGIMERGKGCEVEVDESGST 466
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Pred. No. 1.2e-99
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Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Graessle S., Dangl M., Haas H., M
Walton J.D., Loidl P., Brosch G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Eurotiales; Trichocomaceae; Emericella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9P4F5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochim, Biophys. Acta 1492:120-126(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of two putative histone Aspergillus midulans.";
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                                                                                                             RDGIDDVSYKSIFEPVIKSVMEMYRPEAVVLQCGGDSLSGDRLGCFNLSMRGHANCVKYV
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    NMDNANTREYLDKIRTQVVENLKRTAFAPSVQMTDVPRE---PLVDGMDDEAEAALD-DL
                               NMENKNSROMLEEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDS
                                                          KSFNLPTLIVGGGGYTMRNVARTWAFETGILVGDNLGSELPYNDYYEYFAPDYELDVRPS
                                                                                   RSFNVPLLLLGGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPS
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Q9JM08;
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01-OCT-2000
01-JUN-2001
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PRINTS; PR01270; HDASUPER.
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MEDLINE=20391214; PubMed=10542131;
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                                                                                                               VARCWTYETSLLVEEAISEELPYSEYFEYFAPDFTLHPDVSTRIENQNSRQYLDQIRQT1
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56.1%; Pred. No. 1.8e-98;
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Sciurognathi; Muridae;
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Best Loca
Matches
 059702;
059702;
01-AUG-1998
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01-OCT-2000
01-JUN-2001
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InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
SEQUENCE 428 AA; 48737 MW; EDE9F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HISTONE DEACETYLASE-3.
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*Isolation and characterization
                                                                                                                                                                                                                                                                                                  316
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   (TrEMBLrel.
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                                     PRELIMINARY;
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   07,
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Last sequence up
Last annotation
   Created)
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Pred. No. 2
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Sciurognathi; Muridae;
                                     PRT;
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2.2e-98;
hes 92; Indels
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; Murinae; Mus
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Best Local :
            062339 PRELIMINARY; PRT; 46: 062339; 062343; 01-AUG-1998 (TREMBLrel. 07, Created) 01-NOV-1998 (TREMBLrel. 08, Last seq; 01-JUN-2001 (TREMBLrel. 17, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genetics 150:563-576(1998).
EMBL; AL023589; CAA19053.1;
EMBL; AF064206; AAD05211.1;
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Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000286; His_deacetylse
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
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Grewal S.I., Bonaduce M.J., Klar A.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moestl D., Duesterhoeft A.;
Submitted (MAY-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyne M., Wood V., Rajandream M.A., Moestl D., Duesterhoeft A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
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                                                                                                                                                                      IENLRNLSFAPSVQMHKTPGD 384
                                                                                                                                                                                                      LHNLSKLQHAPSVPFQERPPD
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PROTEIN
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            Last sequence update)
Last annotation update)
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Last annotation updat
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Pred. No. 1
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l.1e-96;
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Best Local Similarity
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EMBL; Z81108; CAB03240.1; -
EMBL; Z81106; CAB03240.1; -
EMBL; Z81106; CAB03224.1; -
EMBL; Z81108; CAB03224.1; -
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thistory M., Morting Y., Watchen R., Sulston D.,
Thistory M., Sonnhammer E., Staden R., Sulston D.,
Thistory M., Sonnhammer E., Staden R., Sulston D.,
Thistory M., Smith A., Sonnhammer E., Staden R., Sulston D.,
Thistory M., Morting T., Thomas K., Watchen R., Sulston D.,
Thistory M., Sonnhammer E., Staden R., Sulston D.,
Thistory M., Sonnhammer E., Staden R., Sulston D.,
Thistory M., Morting T., Thomas K., Watchen R., Sulston D.,
Thistory M., Sonnhammer E., Staden R., Sulston D.,
Thistory M., Sonnhammer E., Staden R., Sulston D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                LHNLSKLQHAPSVPFQ--ERPPDTETPEVDE----DQEDGDKRWDP-DSDMDVDDDRKPI
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-SAEFYDGQEPETKNIQSMK
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Pred. No. 1
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1.9e-96;
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Best Local :
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Q9C1C6;
01-JUN-2001
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wegener S., Walton J.D.;
"HDC2, a histone deacetylase gene related to F
filamentous fungus Cochliobolus carbonum.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
EMBL; AF349677; AAK35180.1;
SEQUENCE 648 AA; 70940 MW; 242147C293D4EAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cochliobolus carbonum (Bipolaris zeicola).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Pleosporales; Pleosporaceae; Cochliobolus.
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                         GVEEASVKMEEEGTNKGGAEQAFPP 499
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PVPEAALETAPE - - - - TAPAAAPP
                                                                                                                                          WDPDSDMDV
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                                                                                                                                                                                                                            {\tt YVKSFGVPVIVLGGGGYTMRNVARTWAYETGELVSQKMSKQLPFNDYYEYFAPDYELDVR}
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                                                       AAPADALDLMED I NGGSAVSTRQPSAGAKSRTQTPAAAAEQEVDKDGDVDMDAPVPESAPE
                                                                                                              MDADENROVRMTQRQRDKQ1EHDGELYBASDDEDYKNNLGVRAQPGVKKRRN1TDFPNPN
                                                                                                                                                                     PSNMENANSHDYLHKIKSAVIENIRRTGR-PSVEAFTTIPDVPTALGRAMDSDAEDEEDD
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-2001 (TrEMBLrel.
E DEACETYLASE 2.
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                                                                                 -PDTKDKDGLKGIMERGKGCEVEVDESG----STKVTGVNPV
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Last annotation update)
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OM protein - protein search, using sw model
                                                           April 26, 2002, 17:52:17; Search time 17.07 Seconds
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(without alignments)
1076.103 Million cell updates/sec
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Title: Perfect score:

US-09-645-337-2 2722 1 MDTGGNSLASGPDGVKRKVC.....KMEEEGTNKGGAEQAFPPKT 501

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1544 1538 1520 1521 1521 1527 1494 1494 1465.5 1392 1392 1393 1373 1373 1373 1373 1373 1373 1373	2722 1986.5 1554	Score
99.81111.892.932.603.834.44.46.77.99.99.81.834.44.46.79.99.99.81.834.44.46.79.99.99.99.99.99.99.99.99.99.99.99.99.		Query Match I
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Query Match 100.0%; Score 2722; DB 1; Best Local Similarity 100.0%; Pred. No. 1.2e-203; Matches 501; Conservative 0; Mismatches 0;

Length 501; Indels

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107	108	108	111.5	112	117	127.5	185	208	230	238	254
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YGX7_YEAST	SEC7_YEAST	NPM_CHICK	CYL2_BOVIN	HIBN_XENLA	ANK1_MOUSE	HOS3_YEAST	APHA_MYCRA	Y245_SYNY3	Y535_METJA	YB94_METTH	YLFN_CAEEL
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                                                                                                                                                                                                                                                                                       ROSSI V., Hartings H., Motto M.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE NOTERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
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P56521;
                                                                                                                                                                                                      This
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20-AUG-2001 (Rel. 40, Last annotation
PROBABLE HISTONE DEACETYLASE (RPD3 HO)
Hydrolase;
SEQUENCE
                           PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                    InterPro; IPR000286; His_deacetylse Pfam; PF00850; Hist_deacetyl; 1.
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                                                                                                             non-profit institutions as long as its content
and this statement is not removed. Usage by ar
requires a license agreement (See http://www.isb
an email to license@isb-sib.ch).
 Nuclear protein
513 AA; 57546 P
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HDA1_MOUSE STAN

009106; p97476;

01-NOV-1997 (Rel. 3

01-NOV-1997 (Rel. 3

20-AUG-2001 (Rel. 4
                                                                                                                                                                        TISSUE-Fibroblast;
MEDLINE-97415582; PubMed-9271381;
Bartl S. Taplick J., Lagger G.,
                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
20-AUG-2001 (Rel. 40,
HISTONE DEACETYLASE 1
                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                   HDAC1
                                                                             Johnson C.A.;
Submitted (SEP-1997)
-!- FUNCTION: RESPONS
                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                       inducible gene.";
Mol. Cell. Biol.
                                                                                                                                                               "Identification of mouse
                                                                                                                                                                                                                                   NCBI_TaxID-10090;
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FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4). HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY SIMILARITY).

FUNCTION: ACTS AS A TRANSCRIPTIONAL REPRESSOR SUBUNIT: FORMS A COMPLEY NATE.
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377; Conserv
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Chordata;
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Pred. No. 1.36
                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleosto
Sciurognathi; Muridae; Murinae;
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Best Local :
HDA1_HUMAN STANDARD; I
Q13547; Q92534;
Q1-NOV-1997 (Rel. 35, Created)
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PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
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SUBCELLULAR LOCATION: NUCLEAR
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHER LEVELS IN THYMUS
AND TESTIS AND LOWER LEVELS IN LIVER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGVEEASVKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEE 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTI 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTKRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGEGGRKNSSNFKKAKRVKTE----DEKEKD-----PEEKK----EVTEEEKTKEEKPEA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVDDDRKPIPS----RVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTKVTGVNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLHNLSKLQHAPSVPFQERPPDTETPEV-DEDQEDGDKRWD------PDSDM 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIKQR 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEEIRND 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGGGGYTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIM 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGVEE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYHSDDYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REHADDYVSFLRSITPETQQDQIRQLKRENVGEDCPVFDGLYSFCQTYAGGSVGGSVKLN 133
                                                                                                                                                                                                                                                                                                                                                       KGVKE-EVKL 481
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60.0%;
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                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPD3, a transcription factor in Saccharomyces cerevisiae.";
Cytogenet. Cell Genet. 73:130-133(1996).
-!- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, 20-AUG-2001 (Rel. 40, HISTONE DEACETYLASE 1
                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00850; Hist_deacetyl; PRINTS; PR01270; HDASUPER. PRINTS; PR01271; HISDACETLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vo
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HDAC1 OR RPD3L1
                                                                                                                                                                                                                                                                                                                     Hydrolase; Nuclear CONFLICT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U50079; AAC50475.1; -. EMBL; D50405; BAA08909.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Fetal lung;
MEDLINE=96244606; PubMed=8646880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulator Rpd3p.";
Science 272:408-411(1996).
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                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                            MIM; 601241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Akiyama T., Nakamura Y.;
"Isolation and mapping of a human gene (RPD3L1) that is homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Furukawa Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taunton J., Hassig C.A., Schreiber S.L.;
"A mammalian histone deacetylase related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96185499; PubMed=8602529;
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                                 134
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                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: NUCLEAR.
TISSUE SPECIFICITY: UBIQUITOUS, WITH HIGHER LEVELS IN HEART,
PANCREAS AND TESTIS, AND LOWER LEVELS IN KIDNEY AND BRAIN.
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
FAMILY. HD SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS. SUBUNIT: FORMS A COMPLEX WITH RBAP48 AND ALSO WITH THE HISTON ACETILITANSFERASE P/CAF AND THE ADAPTATOR PROTEIN P300. ALSO A COMPLEX WITH SIN3 AND SAP18. INTERACTS WITH TGIF.
                                                                                                                                  KQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGVEE
                  HGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEE
                                                                  KYHSDDYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLN
                                                                                                   RFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLN 133
                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                           IPR000286; His_deacetylse.
                                                                                                                                                                                                                                                                                                    482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawakami T., Sudo K., Inazawa J., Matsumine
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                    55103 MW;
                                                                                                                                                                                                                         56.7%; Score 1544; DB 1; 59.4%; Pred. No. 2.6e-112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
(HD1).
                                                                                                                                                                                                              67;
                                                                                                                                                                                                                                                                                                 W -> R (IN REF. 2).
4; 4D35B7C1ED7838D6
                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                    CRC64;
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                                                                                                                                                                                                                                             Length 482;
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RESULTING AND PROPERTY OF THE 
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P56517;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seque
20-AUG-2001 (Rel. 40, Last annot
HISTONE DEACETYLASE 1 (HD1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sun J.M., Chen H.Y., Davie J.R.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-i-FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; (
Archosauria; Aves; Neognathae;
   InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                  entitles requires a
                                                                                                                                                                                                                                                                                                 modified and this statement is not removed.
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                                                                                                                    EMBL; AF044169; AAC00504.1; -
                                                                                                                                                                               EMBL; AF039751; AAB96923.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
SUBUNIT: FORMS A COMPLEX WITH RBAP48 (BY SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC
                                                                                                                                                                                                                                                                                                                                                           European
                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation EDUropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAMILY. HD SUBFAMILY 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGULATION, CELL CYCLE PROGRESSION
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                                                                                                                                                   AF043328;
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                                                                                                                                                                                                                                   equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
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Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
(HD1).
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SEQUENCE
                                                    SEQUENCE FROM N.A.

Patterton D., Wolffe A.P.;

Patterton D., Wolffe A.P.;

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

PUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                           HD12_XENLA STANDARD; PRT; 480 AA. 042227; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) PROBABLE HISTONE DEACETYLASE 1-2 (HD1) (RPD3 | Xenopus laevis (African clawed frog)).
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DOMAIN
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DOMAIN
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                      NCBI_Tax1D=8355;
                                                                                                                                                                     Xenopodinae;
                                                                                                                                                                                  Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246
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Local Similarity
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REGULATION, SIMILARITY).
SUBCELLULAR
SIMILARITY:
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                                           CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS
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 HISTONE
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No. 7
                SIMILARITY)
 DEACETYLASE
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Best Local
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                                                                                             HISTONE DEACETYLASE) (HDM) (AB21). Xenopus laevis (African clawed frog).
                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-JUC-1998 (Rel. 36, Last annotation update)
PROBABLE HISTONE DEACETYLASE 1-1 (HD1) (MATERNALLY-EXPRESSED
                                                                                                                                                                                                  Q91695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                  HD11_XENLA
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                                                        Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                     426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLN 13:
                                                                                                                                                                                                                                                                                                    EGEGGRKNVANFKKVKRVKTE-EEKEGEDKKDVKEEEKAKDEKTD 469
                                                                                                                                                                                                                                                                                                                                     DVDDDRKPIPS -- RVKREAVEPDTKDKDGLKGIMERGKGCEVEVD
                                                                                                                                                                                                                                                                                                                                                                                                     LLHNLSKLQHAPSVPFQERPPDT-ETPEVDEDQEDGDKRWD------PDSDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEEIRND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TKVMEMFQPSAVVLQCGADSLSGDRLGCFNLTIKGHAKCVEFIKTFNLPMLMLGGGGYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKVMEIFRPGAVVLOCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGGYTI 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KQQTDISVNWSGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVVYIDIDIHHGDGVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYHSDDYIKFLRSIRPDNMSEYSKOMORFNYGEDCPYFDGLFEFCQLSTGGSVASAVKLN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTKKKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKASAEEMT 65
                                                                                                                                                                                                                                                                                                                                                                     LFENLRMLPHAPGVQMQAIPEDSVHDDSGEEDEEDPDKRISIRSSDKRIACDEEFSDSED
                                                                                                                                                                                                                                                                                                                                                                                                                                      RNVARCWTYETAVALDSEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIKQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFYATDRYMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000286; His_deacetylse
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                                            Xenopus
                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.9%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54892 MW; CA92DE34D36E39E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1521; DB 1;
Pred. No. 1.6e-110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-GLY
                                                                                                                                                                                                                  PRT;
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Gene 198:275-280(1997).

-!- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01270; HDASUPER. PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00850; Hist_deacetyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X78454; CAA55211.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98036059; PubMed=9370292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000286; His_deacetylse
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SUBCELULIAR LOCATION: NUCLEAR (BY SIMILARITY).

TISSUE SPECIFICITY: OOCYTE.

DEVELOPMENTAL STAGE: ACCUMULATES IN PREVITELLOGENIC OOCYTES
MAINTAINED AT CONSTANT LEVEL THROUGHOUT OOGENESIS AND INTO
EMBRYCGENESIS. DECLINES THROUGH GASTRULA TO NEURULA. NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THAN OVARY.
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC
FAMILY. HD SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DETECTABLE BETWEEN NEURULA AND TAILBUD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                         RFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLN 133
                                                                                                                                                                  SKVMEMFQPSAVVLQCGADSLSGDRLGCFNLTIKGHAKCVEFIKTFNLPLLMLGGGGYTI
                                                                                                                                                                                                                                                      AFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                            GTKKKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIFRPHKASAEDMT 65
                                                                                                                      RNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEEIRND
                                                                                                                                                                                                  {\tt GKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTI}
                                                                                                                                                                                                                                  AFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYALRDGIDDESYEAIFKPVM
                                                                                                                                                                                                                                                                                                       KQQTDISVNWSGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVVYIDIDIHHGDGVEE
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                                 LFENLRMLPHAPGVQMQAVAEDSIHDDSGEEDEDDPDKRISIRSSDKRIACDEEFSDSED
                                                                                                   RNVARCWTYETAVALDSEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIKQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    non-profit institutions as long as its content
RKPIPS -- RVKREAVEPDTKDKDGLKGIMERGKGCEVEVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54747 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1520; DB 1;
Pred. No. 1.9e-110;
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; 7B831822235DADB5 CRC64;
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                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yang W.-M., Inouye C.J., Zeng Y., Bearss D., Seto E.;
"Transcriptional repression by YY1 is mediated by interaction with a mammalian homolog of the yeast global regulator RPD3.";
Proc. Natl. Acad. Sci. U.S.A. 93:12845-12850(1996).

1- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N.TERMINAL PART OF THE CORE HISTORES (H2A. H2B. H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN).
HDAC2 OR YY1BP
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00850; Hist_deacetyl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97075080; PubMed-8917507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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20-AUG-2001
                                                                                                                                                                                                                                                                                                                  Hydrolase; Nuclear protein.
DOMAIN 300 303
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000286; His_deacetylse.
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                                 121
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                                                                                         61 TAEBMTKYHSDEYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVA 120
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                                                                                                                                                                                                                                                     Match
                                                                                                                                                                                                                                      ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
                                                                                                                                                                                                                                                                                                                                                                                                        MGI:1097691; Hdac2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: FORMS TRANSCRIPTIONAL REPRESSOR COMPLEXES BY AT LEAST WITH THE ZINC-FINGER TRANSCRIPTION FACTOR YYL. SUBUNIT: FORMS A HETEROLOGOUS COMPLEX WITH YYL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY)
GDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHL
                                                GSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL
                              GAVKLNRQQTDMAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHH
                                                                                                                                                                                      LASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPA
                                                                                                                         RERDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVG
                                                                                                                                                        MAYSQGGGKKKVCYYYDGDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit institutions as long a and this statement is not removed.
                                                                                                                                                                                                                                                                                                  488
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(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
(CETYLASE 2 (HD2) (YY1 TRANSCRIPTION FACTOR BINDING
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                300
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                                                                                                                                                                                                                                                                                                  55302 MW;
                                                                                                                                                                                                                                   55.6%;
                                                                                                                                                                                                                      82;
                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                POLY-GLY
                                                                                                                                                                                                                                     Score 1513.5;
Pred. No. 6.1
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                                                                                                                                                                                                                                                                                                B9843D24A775157C CRC64;
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                                                                                                                                                                                                                                  .5; DB 1;
5.1e-110;
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GVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLC

Query Match Best Local Matches

Similarity

55.4%;

Conservative

75;

Score 1507; Di Pred. No. 2.4e 75; Mismatches

.4e-1

DB 109;

Length

Indels

26;

Gaps

6;

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15-JUL-1998
20-AUG-2001
                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
 Hydrolase;
SEQUENCE
                               PRINTS; PR01270; HDASUPER. PRINTS; PR01271; HISDACETLASE.
                                                            InterPro; IPR000286; His_deacetylse
Pfam; PF00850; Hist_deacetyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strongylocentrotus purpuratus (Purple sea urchin) Eukaryota; Metazoa; Echinodermata; Eleutherozoa; I
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                                                                                              EMBL; AF032919; AAB87685.1; -
                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics That into There are no restrictions on its the Purpose and Institute That into There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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Nuclear protein.
576 AA; 64078 MW;
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(Rel. 36, Last sequence up
(Rel. 40, Last annotation
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 B3D11A844A2088E9 CRC64;
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15-JUL-1998
20-AUG-2001
HISTONE DEAC
                                                                                                                                                                                              MEDLINE-97075080; PubMed-8917507;

Yang W.-M., Inouye C.J., Zeng Y., Bearss D., Seto E.;

Yang M.-M., Inouye C.J., Zeng Y., Bearss D., Seto E.;

"Transcriptional repression by YY1 is mediated by interaction with a mammalian homolog of the yeast global regulator RPD3.";

Proc. Natl. Acad. Sci. U.S.A. 93:12845-12850(1996).

-1- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE UNIVERSITY OF THE CORE HISTONES (H2A, H2B, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
This SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                          TISSUE-Breast;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HDA2_HUMAN
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                                                                                                               FUNCTION: FORMS TRANSCRIPTIONAL REPRESSOR COMPLEXES BY ASSOCIATING WITH MAD, SIN3, YYI AND N-COR.
SUBUNIT: FORMS A HETEROLOGOUS COMPLEX AT LEAST WITH YY1.
SUBCELLULAR LOCATION: NUCLEAR.
                                                    LUNG.
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
                                             FAMILY.
                                                                                                  TISSUE SPECIFICITY: WIDELY
                                                                                                                                                                                    SIMILARITY).
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1998 (Rel. 36, Last sequence update)
2001 (Rel. 40, Last annotation update)
DEACETYLASE 2 (HD2).
                                               HD SUBFAMILY 1.
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the Swiss Institute of Bioinformatics

and the

EMBL outstation

Ephydroidea; Drosophilidae; Drosophila. NCBI_TaxID=7227;

Drosophila melanogaster (Fruit fly). Eukaryota; Metazoa; Arthropoda; Tracheata; He Pterygota; Neoptera; Endopterygota; Diptera;

Hexapoda; Insecta;

Brachycera;

Muscomorpha

RPD3 OR HDAC1

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Best Local S
Matches 277
                                                                                                   HDAC_DROME STANDARD: PRT: 520 AA (994517; 017429; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation updat PROBABLE HISTONE DEACETYLASE (HD) (DRPD3).
                                                                                                                                                                                                    DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000286; His_deacetylse. Pfam; PF00850; Hist_deacetyl; 1. PRINTS; PR01270; HDASUPER. PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U31814; AAC50814.1; -. MIM; 605164; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
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Pred. No. 26
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[2]
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PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y09258; CAA70455.1; ---
EMBL; RF026649; AAC23917.1; ---
EMBL; EB900015805; RPd3.
InterPro; IPR000286; His_deacetylse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spierer P.; "The histone deacetylase RPD3 counteracts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00850;
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185
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                                                                                                                                                                                                                                                                                                                                                      6
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mitted (NOV-1997) to the EMBL/GenBank-DOBJ debases.
FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON
THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
SIMILARITY). IN DROSOPHILA, IT IS INVOLVED IN POSITION-EFFECT
VARIEGATION (PEV) AND IS DIRECTLY INVOLVED IN COUNTERACTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL) SIMILARITY: BELONGS TO THE HISTONE DEACET
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                                           VMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGGYTIRN
                                                                                      YTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNIPLRDGMDDDAYESIFVPIISK
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                                                                                                                                                                                                                    LCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAF 195
                                                                                                                                                                                                                                                             HCDEYVRFLRSIRPDNMSEYNKQMQRFNVGEDCPVFDGLYEFCQLSAGGSVAAAVKLNKQ 124
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384:589-591(1996).
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Pred. No. 3
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E -> D (IN REF. 2).
E -> D (IN REF. 2).
V -> VV (IN REF. 2).
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S -> T (IN REF. 2).
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-i- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE CORE HISTONES (HLA. HLB. H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
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15-JUL-1998 (Rel. 36, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
HISTONE DEACETYLASE 2 (HD2).
                                                                                                                                                                                                                                                                                                                 PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
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15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                               InterPro;
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SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL)
SIMILARITY: BELONGS TO THE HISTONE DEACET
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                             GSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHH 187
                                                                                                                         LASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPA
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                                                             TAEEMTKYHSDEYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVA 120
                                                                                          RERDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVG 127
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                                                                                                                                                                                                                                                                                                                                                               IPR000286; His_deacetylse
                                                                                                                                                                                                                                                                    488 AA;
                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                    300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Chicken).
                                                                                                                                                                                                                                                                                                                                             Hist_deacetyl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neognathae;
                                                                                                                                                                                                                                                                                                 protein.
                                                                                                                                                                                                                                                                    55153 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                       53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TO THE HISTONE DEACETYLASE / ACUC / APHA
                                                                                                                                                                                        81;
                                                                                                                                                                                                     Score 1465.5; DB 1
Pred. No. 3.2e-106;
                                                                                                                                                                                                                                                                                    POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                    4F79B9C0D4A2D065 CRC64;
                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
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                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and the
                                                                                                                                                                                        Indels
                                                                                                                                                                                                                     Length 488;
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3.
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Query Match
Best Local Similarity
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence up
20-AUG-2001 (Rel. 40, Last annotation
PROBABLE HISTONE DEACETYLASE 1.
HDA-1 OR C53A5.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAEEL
                                                                                                                                                                                                                                        InterPro; IPR000286; His_deacetylse
Pfam; PF00850; Hist_deacetyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mortimore B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                   PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                       WormPep; C53A5.3; CE08952
                                                                                                                                                                                                                                                                                                                                   EMBL; Z81486; CAB03984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
SIMILARITY: BELONGS TO THE HISTONE DEACETYLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAMILY. HD SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EASVKMEEEGTNKGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIPSRVKREAVEPDTKDKD-----GLKGIMERGKGCE---VEVDESGSTKVTGVNPVGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDED--QEDGDKRWDPDSDMDVDDDRK 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSROML
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                                                                                                                                                                                                                                                                                                                                                                                               s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                   Nuclear protein.
                                                                                                                          461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                             52137
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   51.1%;
57.2%;
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                                                                                                                          MW.
   Score 1392;
Pred. No. 1
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                                                                                                                          9A104E88C5A1C07A CRC64;
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      .5e-100;
                                  DB 1;
                               Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APHA
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P56520;
15-JUL-1998
                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collal between the Swiss Institute of Bioinformatics and the EMBL outs the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                               CHICK
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                        Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken)
                                                                                                                                                                                                                                                                                                                                                                                                    HDAC3
                                                                                                                                                                                                                                                                                                                                                                                                               HISTONE DEACETYLASE
                                                                                                                                                                                                                                                                                       Takami Y
                                                                                                                                                                                                                                                                                                                                                                                                                           20-AUG-2001
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                                                                                                                                                                       REGULATION, CELL CYCLE SIMILARITY).
SUBCELLULAR LOCATION: N
SIMILARITY: BELONGS TO
                                                                                                                                                               FAMILY. HD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VDIDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGGSLAAATKLNKQKVDIAINWMGGLHHAKKSEASGFCYTNDIVLGILELLKYHKRVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAGGSVGGSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENSSDMLAKLQTDVIANLEQLTFVPSVQMRPIPEDALSALNDDSLIADQANPDKRLPPQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPLMMVGGGGYTPRNVARCWTYETS I AVDKEVPNELPYNDYFEYFGPNYRLH I ESSNAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VDIDVHHGDGVEEAFYTTDRVMTVSFHKYGDFFPGTGDLKDIGAGKGKLYSVNVPLRDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt IFRPFPASFEDMTRFHSDEYMTFLKSANPDNLKSFNKQMLKFNVGEDCPLFDGLYEFCQL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLKPFPARERDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259;
                                                                                                                                                                                                                                                                                                                                                                    Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 36, Last sequence up
(Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                             SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                          BELONGS TO THE HISTONE DEACETYLASE / ACUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DSDMDVDDDRKPIPSRVKREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      36, Created)
                                                                                                                                                                                                                                                                                                                                                         Neognathae;
                                                                                                                                                                                                                                                                                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KRRVAYYYDSNIGNYYYGQGHVMKPHRIRMTHHLVLNYGLYRNLE
                                                                                                                                                                                                                                                                                                                                                                                                              (HD3).
                                                                                                                                                                                          NUCLEAR
                                                                                                                                                                                                                  PROGRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 89
                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                  AND DEVELOPMENTAL
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                                                                                                                    EMBL outstation
                                                                                                                                                                                                                  EVENTS
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                                                                                                                                                                          / APHA
                                                                                                                     a collaboration
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EMBL;

AF039753; AAB96925.1; -

IPR000286; His_deacetylse

InterPro;

PF00850;

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                                                                                                                                                                                                                                                                                                                             HDA3_HUMAN STANDARD; PRT (015379; 041268; 09UEVO; 09UEI5; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequen 20-AUG-2001 (Rel. 40, Last annota HISTONE DEACETYLASE 3 (HD3) (RPD3
                                                                                                                                                                                                                                                                                                                                                                                                                                HUMAN
additional member of the human histone deacetylase gene family."; J. Biol. Chem. 272:28001-28007(1997).
                                                                                                                                                                  Dangond F., Hafler D.A., Tong J.K., Gullans S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS: PR01270; HDASUPER.
PRINTS: PR01271; HISDACETLASE
                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE-T-cell, and Spleen;
MEDLINE-98125547; PubMed-9464271;
                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                          Yang W.-M., Yao Y.-L., Sun J.-M., Davie J.R., Seto E.; "Isolation and characterization of cDNAs corresponding to
                                                                         TISSUE-Fibroblast;
                                                                                                                    "Differential display cloning of a novel human histone (HDAC3) cDNA from PHA-activated immune cells."; Blochem. Blophys. Res. Commun. 242:648-652(1998).
                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                             MEDLINE-98010646;
                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1 AND
                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSDMDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAFY 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FENLKMLNHAPSVQIHDVPSDLLSYDRTDEPDPEERGSEENYSRPEAANEFYDGDHDNDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLLGGGGYTIRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTVAYFYDPDVGNFHYGAGHPMKPHRLALTHSLVLHYGLYKKMIVFKPYQASQHDMCRFH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear protein. 428 AA; 48901 MW; 42E32733AD2BBF07 CRC64;
                                                                                                                                                                                                                                                                                                                                    (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
CETYLASE 3 (HD3) (RPD3-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                             PubMed-9346952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.8%;
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                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                         2)
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                                                                                                                                                                                Randall J., Kojima
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                                                                                                                                                                                 R., Utku N.
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SEDYIDFLQRVSPTNMQGFTKSLNAFNVGDDCPVFPGLFEFCSRYTGASLQGATQLNNKI

ADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHGL 136 KTVAYFYDPDVGNFHYGAGHPMKPHRLALTHSLVLHYGLYKKMIVFKPYQASQHDMCRFH

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STATE OF THE STATE OF STATE OF
                                                                                                                                           Query Match
                                                                                      Matches
                                                                                                                   Best
                                                                                                                                                                                                                              CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF005482; AAB87752.1; -.
EMBL; AF039703; AAC98927.1; -.
EMBL; AF0596503, AAC26509.1; -.
EMBL; AF053138; AAC08351.1; -.
EMBL; AF053137; AAC08351.1; JOINED.
EMBL; AF053137; AAC08352.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U66914; AAC52038.1; -. EMBL; U75697; AAB88241.1; -. EMBL; U75696; AAB88240.1; -. EMBL; AF005482; AAB87752.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.ish-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstatt the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -II- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (42A, 42B, 43 AND 44). HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS.
-II- FUNCTION: MAY PARTICIPATE TO THE REGULATION OF TRANSCRIPTION THROUGH ITS BINDING MITH THE ZINC-FINGER TRANSCRIPTION FACTOR YYLLINCREASES YYL REPRESSION ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=99162406; PubMed=10051405; Mahlknecht U., Emiliani S., Najfeld V., Young S., V Mahlknecht U., Emiliani S., Najfeld V., Young S., V "Genomic organization and chromosomal localization histone deacetylase 3 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=9816945; PubMed=9501169;
Emiliani S., Fischle W., van Lint C., Al-Abed Y.,
"Characterization of a human RPD3 ortholog, HDAC3
Proc. Natl. Acad. Sci. U.S.A. 95:2795-2800(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lynch E.D., Lee M.K., King M.-C.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 605166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00850;
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                                                                                                                Local
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ALTERNATIVE PRODUCTS: 2 ISOFORMS: 1/RPD3-2B (SHOWN HERE)
2/RPD3-2A; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: WIDELY EXPRESSED.
SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / IFAMILY. HD SUBFAMILY 1.
RKVCYFYDPEVGNYYYGGGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRFH 76
                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000286; His_deacetylse
                                                                                                                                                                                                                     359
428
                                                                                                                                                                                                                                                                                                                                            Nuclear protein; Alternative splicing
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Hist_deacetyl;
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                                                                                                                                                                                                                                                            359
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                                                                                                                                                                                                                                 48847
                                                                                                                56.6%;
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                                                                                      73;
                                                                                                                                                                                                                           ISOFORM 2).
R -> L (IN REF. 1)
; 94485C1EBDCF5AD0
                                                                                                                                           Score
                                                                                                                Pred.
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                                                                                      Mismatches
                                                                                                                No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                   4e-99
                                                                                                                                           DB
                                                                                                                                  1;
                                                                                      90;
                                                                                                                                                                                                                                 CRC64;
                                                                                                                                           Length
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                                                                                      Indels
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    415 DSDMDV 420
                             123 ESDVEI 428
                   363 FENLKMLNHAPSVQIHDVPADLLTYDRTDEADAEERGPEENYSRPEAPNEFYDGDHDNDK 422
                      -----PEVDEDQEDGDKRWDP 414
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Search completed: April 26, 2002, 17:57:50 Job time: 333 sec

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Title:

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OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 MDTGGNSLASGPDG
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Comp
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pir2:*
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                                                                                                                                                                                                                                                              Length
                                                   DB
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T40300
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acetylpolyamine am	HB3469	ν.	346	7.2	196.5	45	
probable acetylpo	в83605	N	344	7.2	197	44	
histone deacetylas	H75470	2	301	7.4	201	43	
acetylpolyamine am	S74557	<u>ب</u>	304	7.6	208	42	
hypothetical prote	T05998	2	359	8.2	223.5	41	
histone deacetylas	F81178	N	369	8.2	224.5	40	
histone deacetylas	D82126	N	306	ω ω	227	39	
acetylpolyamine am	G64366	_	343	8.4	230	38	
hypothetical prote	A81926	N	385	8.5	230,5	37	
hypothetical prote	T27101	2	517	8.7	236	36	
acetylpolyamine am	C69026	_	331	8.7	238	ω G	
hypothetical prote	T32425	N	796	8.9	243.5	34	
glnA 3'-region hyp	B47050	N	310	9.6	261.5	i i	
hypothetical prote	н71071	_	335	9.7	264	32	
acetoin utilizatio	Н84173	2	338	10.0	271.5	31	
probable histone o	T13964	Ν	1095	10.1	2/5.5	30	

histone deacetylase (EC 3.5.1.-) F20D10.250 - Arabidopsis thaliana

A:Map position: 4
A:Introns: 176/3; 323/3; 400/3; 424/2; 443/3; 467/3
C:Superfamily: RPD3 protein; RPD3/acuC homology
C:Keywords: hydrolase
F:21-320/Domain: RPD3/acuC homology <RAH> R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, February 1999
A;Reference number: 215420 N;Alternate names: protein F20D10.250
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 *sequence_revision 23-Apr-1999 *text_change 12-Nov-1999
C;Accession: T05640 δÃ Ş рь γQ 5 밁 밁 δÃ Db 밁 A;Cross-references: EMBL:AL035538; GSPDB:GN00062; ATSP:F20D10.250 A;Experimental source: cultivar Columbia; BAC clone F20D10 A; Molecule type: DNA A; Residues: 1-501 <BEV> Š A; Gene: ATSP: F20D10.250 C; Genetics: A; Accession: T05640 Matches Query Match Best Local Similarity 121 301 241 181 181 301 121 YAGGSVGGSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLY 61 61 1 MDTGGNSLASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQ 1 MDTGGNSLASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQ VPLLLLGGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMEN 360 VDIDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGI VLKPFPARERDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQT 120 YAGGSVGGSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLY DDESYHLLFKPIMGKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFN VDIDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGI VLKPFPARDRDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQT VPLLLLGGGGYT I RNVARCWCYETGVALGVEVEDKMPEHEYYEY FGPDYTLHVAPSNMEN DDESYHLLFKPIMGKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFN 500; Conservative 99.9%; Score 2719; DB 2; 99.8%; Pred. No. 1.1e-202; vative 1; Mismatches 0; Length 501; Indels 0; Gaps 240 240 180 180 120 60 60 300 300 0;

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A;Cross references: EMBL:AF035815; NID:g2665839; PIDN:AAC50038.1;
A;Experimental source: strain W22
C;Genetics:
A;Gene: rpd3
C;Superfamily: RPD3 protein; RPD3/acuC homology
C;Keywords: hydrolase
F;27-325/Domain: RPD3/acuC homology <RAH>
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A; Residues: 1-513 <ROS>
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A;Title: Identification and characterisation of an RPD3 homologue
A;Reference number: 214321; MUID:98307342
A;Accession: T01413
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                                               DHKAVEESSRRSILGIKIKREFGENATRVQDGGR-VASEHRGLEPMAEDIGSSKQAPQAD 48.
                                                                                                                                    NSRQMLEEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDSDMDVD
                                                                                                                                                                                                    PLLLLGGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENK
                                                                                                                                                                                                                                                     DESYQSLFKPIMGKVMEVFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVRYMRSFNV
                                                                                                                                                                                                                                                                       DESYHLLFKPIMGKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNV
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                                                                             DD------RKPIPSRVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTK---VTG
                                                                                                               {\tt NTRQQLDDIRS----KLSKLRHAPSVHFQERVPDTEIPEQDEDQDDPDERHDPDSDMEVD}
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                                                                                                                                                                                    PLLLLGGGGYTIRNVARCWCYETGVALGQEPEDKMPVNEYYEYFGPDYTLHVAPSNMENK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGGNSLPSVGPDGQKRRVCYFYDPDVGNYYYGQGHPMKPHRIRMTHSLLARYGLLNQMQV 67
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75.2%;
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A; Residues: 1-480 <LAD>
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A; Accession: S60381
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          A;Cross-references: EMBL:Z81486; PIDN:CAB03984.1; GSPDB:GN00023;
                            A; Residues:
                                          A; Molecule type: DNA
                                                                           A; Accession: T20163
                                                                                                                                  R; Mortimore,
                                                                                                                                               C; Accession:
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RPD3 protein homolog - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 10-Sep-1999
                                                                                                                                                                                                                                    C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
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R;Ladomery, M.R.; Lyons, S.; Sommerville, J.
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                  hypothetical protein C53A5.3 - Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 GVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 KYHSDDYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSAGGSVASAVKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74 RFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLN 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 GTKKKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIFRPHKASAEDMT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKYMEMFQPSAVYLQCGADSLSGDRLGCFNLTIKGHAKCYEFIKTFNLPLLMLGGGGYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKVME1FRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTI 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIM 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGEGGRKNVANFKKVKRVKTE-EEKEGEDKKDVKEEEKAKDEKTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----RKPIPS--RVKREAVEPDTKDKDGLKGIMERGKGCEVEVD 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFENLRMLPHAPGVQMQAVAEDSIHDDSGEEDEDDPDKRISIRSSDKRIACDEEFSDSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLHNLSKLQHAPSVPFQERPPDT---ETPEVDEDQED-----GDKRWDPDSDMDVDDD 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNVARCWTYETAVALDSEIPNELPYNDYFEYFGPDFKLHISPSNMTNONTNEYLEKIKOR
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Pred. No. 6.8e-110;
                                                                                                                             November
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A:Introns: 19/1; 46/3; 94/2; 121/3; 140/3; 159/2; C;Superfamily: RPD3 protein; RPD3/acuC homology C:Keywords: hydrolase; phosphoprotein F;7-307/Domain: RPD3/acuC homology  RRH1> F;232,282,404/Binding site: phosphate (Tyr) (coval)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AF074881
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Mahlknecht, U.; Hoelzer, D.; Bucala, R.; Verdin, E. Blochem. Biophys. Res. Commun. 263, 482-490, 1999
A;Title: Cloning and characterization of the murine histone A;Reference number: JC7102; MUID:99423490
A;Accession: JC7102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
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A:Introns: 58/3; 98/1; 387/1
A:Superfamily: RPD3 protein; RPD3/acuC homology
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A;Map position: 18B3
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A; Residues: 1-424 <MAH>
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Matches 259
                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                            232,282,404/Binding site: phosphate (Tyr) (covalent) *status
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                                            240;
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                             Score 1366; DB 2;
Pred. No. 4.8e-98;
""matches 91;
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                                                                                                                                                                                                                                                                                                                                                             204/1; 231/1; 252/3; 277/2; 307/2;
                                                                                                        Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: JC5834
C; Accession: JC5834
R; Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R; Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R; Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R; Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R; Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R; Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R; Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R; Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R; Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R; Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R; Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R; Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R; Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R; Dangond, P.; Hafler, D.A.; Tong, D.A.; Ton
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A;Title: Differential display cloning of a novel human histone
A;Reference number: JC5834; MUID:98125547
A;Accession: JC5834
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C;Species: Homo sapiens (man)
C;Date: 05-Mar-1998 *sequence_revision 13-Mar-1998 *text_change 12-Nov-1999
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A; Residues: 1-428 < DAN>
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                                                                                                        CDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAFY 196
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Pred. No. 4.9e-98;
'3; Mismatches 91
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A:Cross-references: EMBL:Z46259; NID:g633655; PIDN:CAA86368.1; PID:g854536
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
R:van Dyck, L.; Pascual-Ahuir, A.; Purnelle, B.; Goffeau, A.
Yeast 11, 987-991, 1995
Yeast 11, 987-991, 1995
A:Title: An 8.2 kb DNA segment from chromosome XIV carries the RPD3 and PAS8 genes as d gene for a putative aryl-alcohol dehydrogenase.
A;Reference number: S57391; MUID:96021610
A;Accession: S57393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transcription regulator RPD3 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein NO305; protein YNL330c
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 23-Mar-2001
C;Accession: $22284; $51336; $51285; $55859; $57393; $63313; $63311
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S22284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, Jaquary 1995
A;Description: Sequence analysis of a 13.9 Kb fr
A;Reference number: S51285
A;Accession: S51285
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A;Description: A 8.2 kb DNA segment from chromosome XIV carries the RPD3 and PAS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      덩
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                                                    A; Molecule type: DNA
A; Residues: 1-433 < VAW>
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A; Residues: 1-201 <MAF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, Yeast 11, 567-572, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1.201 <NIC>
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A; Residues: 1-433 < VAN>
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A; Reference number: S51334
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A; Residues: 1-433 <VID>
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          A; Cross-references:
                                                                                                                                                  A;Status: nucleic acid sequence not shown; translation
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;Accession: S2220.;
;Vidal, M.: Gaber, R.F.
;Vidal, M.: Gaber, R.F.
;Accession: Gaber, Gaber,
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EMBL: x83226; NID: 9642335;
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     PIDN:CAA58228.1; PID:g642338
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C;Superfamily: RPD3 protein; RPD3/acuC homology C;Keywords: nucleus; transcription regulation F;23-322/Domain: RPD3/acuC homology <RAHI>
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A;Experimental source: strain S288C
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A; Residues: 1-433 <COS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 KRKYCYFYDPEYGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                              HNLSKLQHAPSVPFQERPPDTE-TPEVDEDQED-----GDKRWDPDSDMDVDDD 423
                                                                                                                                                                                                                                               VMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGGYTIRN
                                                                                                                                                                                                                                                                                                                                                                                                 KCDVAVNYAGGLHHAKKSEASGFCYLNDIVLGIIELLRYHPRVLYIDIDVHHGDGVEEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                        LCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAF 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTDEYIDFLSRVTPDNLEMFKRESVKFNVGDDCPVFDGLYEYCSISGGGSMEGAARLNRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRRVAYFYDADVGNYAYGAGHPMKPHRIRMAHSLIMNYGLYKKMEIYRAKPATKQEMCQF 77
ANLENTKYAPSVQLNHTPRDAEDLGDVEEDSAEAKDTKGGSQYARDLHVEHDNE
                                                                                               VARTWCFETGLLNNVVLDKDLPYNEYYEYYGPDYKLSVRPSNMFNVNTPEYLDKVMTNIF
                                                                                                                                                                                                IMEWYQPSAVVLQCGGDSLSGDRLGCFNLSMEGHANCVNYVKSFGIPMMVVGGGGYTMRN
                                                                                                                                                                                                                                                                                                YTTDRVMTCSFHKYGEFFPGTGELRDIGVGAGKNYAVNVPLRDGIDDATYRSVFEPVIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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55.6%; Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 433;
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  431
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N;Alternate names: cryptic loci regulator protein clr6
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000

histone deacetylase (EC 3.5.1.-) - fission yeast (Schizosaccharomyces pombe) N;Alternate names: cryptic loci regulator protein clr6

R;Lyne, M.; Wood, V.; Rajandream, M.A.; submitted to the EMBL Data Library, May

Barrell, 1998

B.G.; Hilbert,

H.; Moestl, D.;

Duest

C; Accession: T40300; T43796

T40300

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Accession: T40300 A; Reference number: Z21919

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A;Cross references: EMBL:AR064206; NID:g4159996; PIDN:AAD05211.1; PID:g4159997 A;Experimental source: strain 972 C;Genetics: A;Gene: clr6; SPBC36.05c A;Gene: clr6; SPBC36.05c A;Map position: 2 A;Introns: 14/1; 34/3; 51/3; 91/1; 101/2; 116/1; 131/2; 209/3; 240/3; 277/1; 3:C;Superfamily: RPD3 protein; RPD3/acuC homology C;Keywords: hydrolase; transcription regulation
                                                                                                                                                                                                                                                                                                    hypothetical protein R06C1.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t0 C;Accession: T23963; T24071
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A; Residues: 1-405 <LYN>
A; Residues: 1-405 <LYN>
A; Residues: 1-405 <LYN>
A; Residues: EMBL: ALO23589; PIDN: CAA19053.1; GSPDB: GN00067; SPDB: SPBC36.05c
A; Experimental source: strain 972h; cosmid c36
R; Grewal, S.I.; Bonaduce, M.J.; Klar, A.J.
Genetics 150, 563-576, 1998
A; Title: Histone deacetylase homologs regulate epigenetic inheritance of transcript A; Reference number: 222685; MUID: 98429513
A; Accession: T43796
submitted to the EMBL Data Library, October 1996
A; Reference number: Z19837
                                                                                                                                                                A; Status: preliminary; translated from
                                                                                                                                                                                                                                             submitted to the EMBL Data Library,
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A;Molecule type: DNA
A;Residues: 1-405 <GRE>
                                                  R;Kershaw, J.
                                                                    A;Cross-references: EMBL:Z81106; PIDN:CAB03224.1; GSPDB:GN00019; CESP:R06C1.1
A;Experimental source: clone R06C1
                                                                                                                         A; Residues: 1-465 <WIL>
                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                   A; Reference number: Z19824
A; Accession: T23963
                                                                                                                                                                                                                                                                               R; Kershaw,
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Best Local Similarity
Matches 235; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 HIMOWFRPEAVILOCGTDSLAGDRLGCFNLSMKGHSMCVDFVKSFNLPMICVGGGGGYTVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HADDYVSFLRSITPETQQD-QIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNH 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LHNLSKLQHAPSVPFQERPPD 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVARVWTYETGLLAGEELDENLPYNDYLQYYGPDYKLNVLSNNMENHNTRQYLDSITSEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTIR 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKKVSYFYDEDVGNYHYGPQHPMKPHRVRMVHNLVVNYNLYEKLNVITPVRATRNDMTRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FYTTDRVMTCSFHKFGEYFPGTGHIKDTGIGTGKNYAVNVPLRDGIDDESYESVFKPVIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384
                                                                                                                                                                      GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                         15-Oct-1999 #text_change 31-Jan-2000
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A; Map position: 3
A; Introns: 47/3; 8
A; Note: T18B22.80
C; Superfamily: RPD
                                                                 A;Status: pre.....A;Aclecule type: DNA
A;Molecule type: DNA
A;Residues: 1-419 <JOR>
A;Cross-references: EMBL:ALl38652
A;Cross-references: EMBL:ALl38652
A;Cross-references: cultivar Columbia; BAC clone T18B22
                                                                                                                                                                                                                   A;Reference number: Z24467
A;Accession. minimum.
                                                                                                                                                                                                                                                                                                               hypothetical protein T18B22.80 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
                                                                                                                                                                                          A; Accession: T47443
A; Status: preliminary
                                                                                                                                                                                                                                                        R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; submitted to the Protein Sequence Database, February 2000
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A; Introns: 53/3; 212/1; 279/1; 326/1
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                                                                                                                                                                                                                                                                                                C; Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTIRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSRCWLYETAIALNQEVSDDLPLHDYFDYFIPDYKLHIKPLAALSNFNTPEFIDQTIVAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSRVKREAVEPDTKDKDGLK 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENLKQLPHVPSVQMQSISTSCDSIVKTFDEKLIRDHQNDDVRVTQFEEDVQVED-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YTTDRVMTVSFHKHGEYFPGTGDLKDVGAGSGKYYALNVPLRDGVDDVTYERIFRTIMGE
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                                                                                                                                                                                                                                                                                                    T47443
RPD3 protein; RPD3/acuC homology
                                       87/1; 112/1; 185/2; 206/3; 237/3;
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                                       270/1; 286/3; 317/1; 340/3;
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A;Reference number: Z22404; MUID:98452937
A;Accession: T43300
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В
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                                                                                                                                                            A:Description: involved in the melotic ce
C:Superfamily: RPD3 protein; RPD3/acuC ho
C:Keywords: hydrolase
F:30-330/Domain: RPD3/acuC homology <RAC>
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C: Function:
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                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-434 < KIM>
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R;Kim, Y.B.; Honda, A.; Yoshida, M.; Horinouchi,
FEBS Lett. 436, 193-196, 1998

A;Title: Phd1+, a histone deacetylase gene of Sch
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A;Accession: T11643
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                          Query Match
Best Local
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                                    KRKVCYFYDPEVGNYYYGOGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDP---DSDMDVDDD 423
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   KKRVTYHLDEQVGNYHYGDKHPMKPHRITITNHLVMGYGLHNKMSVFSPRMATFGEMSEF
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4; Mismatches 94;
                                                                       Score 1167.5; DB 2;
Pred. No. 1.2e-82;
5; Mismatches 120;
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A:Introns: 45/1; 298/2
C:Superfamily: RPD3 protein: RPD3/acuC homology
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   LGGGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYY-EYFGPDYTLHVAPSNMENKNSR
                                      LKLFESVISGVEENFNPEAIVLQCGSDSLCEDRLGQFALSFNAHARAVKYVKSLGKPLMV
                                                          HLLEKPIMGKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLL
                                                                                                          HHGDGVQEAFNNSDRVMTVSFHRFGQYFPGSGSIMDKGVGPGKYFAINVPLMAAIRDEPY
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hypothetical protein C08B11.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te
                                                                                                 A;Accession: T19067
A;Status: preliminary; translated from GB/EMBL/DDBJ
                              A;Cross-references: EMBL:Z46676; PIDN:CAA86662.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RALEQLRYLGGAPSVQMQQIPPDLTGHLEEEDERLNDEYLDKAVDVRV
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AADISVFHTEDYVNFLQTVTPKLGLTMPDDV--LRQFNIGEDCPIFAGLWDYCTLYAGGS ERDLCRFHADDYVSFLRSITPE---TQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGS 125 PDGADVKKRNVAYYYHKDVGHFHYGQLHPMKPQRLVVCNDLVVSYEMPKYMTVVESPKLD PDGV---KRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPAR 68 Conservative 39.6%; Score 1077; 46.7%; Pred. No. 1 77; Mismatches) DB 2; 165; Length 507; Indels 18; Gaps 138 80

9

364

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A;Cross-references: EMBL:Z72716; NID:g1322818; PIDN:CAA96906.1; PID:g1322819; MIPS:YGL19
A;Experimental source: strain $288C
R;Coglievina, M.; Delneri, D.; Zaccaria, P.; Klima, R.; Bertani, I.; Bruschi, C.V.
submitted to the EMBL Data Library, September 1995
A;Description: A 6.7 kb fragment from chromosome VII of Saccharomyces cerevisiae contain
A;Reference number: $62051
A;Accession: $62051
A;Accession: $62051
A;Roceule type: DNA
A;Residues: 1-351, HSGTHS', 358, 'RIIHFI', 365-452 <COG>
A;Cross-references: EMBL:X91837; NID:g1177627; PIDN:CAA62950.1; PID:g1177634
A;Experimental source: strain FY1679
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable transcription regulator YGL194c - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein G1330 C;Species: Saccharomyces cerevisiae C;Date: 17-May-1996 #sequence_revisiae 17-May-1996 #sequence_revision 17-May-1996 #text_change 20-Jun-2000 C;Accession: S6421; S62051 R;Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Deln submitted to the Protein Sequence Database, May 1996
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A;Map position: 7L
C;Superfamily: RPD3 protein; RPD3/acuC homology
F;30-331/Domain: RPD3/acuC homology <RAH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-452 <BRU>
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A; Accession: S64211
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                                          LIMTFKPTLIVQQCGADSLGHDRLGCFNLNIKAHGECVKFVKSFGLPMLVVGGGGYTPRN
                                                                                                                                                                                                                                                             CDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKOHERVLYVDIDIHHGDGVEEAFY 196
                                                                                                                                                                                                                                                                                                                                                                                                                                     KVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRFHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RKPIPSRVKREA-VEPDTKDKDGLKGIMERGKGCEVEVDESGSTKVTGVNPVGVEEASVK 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGGGGTTLRNVARCWALETGVILGLRMDDEIPGTSLYSHYFTPRLLRPNLVPKMNDANSA 378
VARCWCYETGVALGVEVEDKMPEH-EYYEYFGPDYTLHVAPSNM-ENKNSRQMLEEIRND 373
                                                                                VMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTIRN 315
                                                                                                                               TTDRVFTLSFHKYNGEFFPGTGDLTEIGCDKGKHFALNVPLEDGIDDDSYINLFKSIVDP
                                                                                                                                                                     ATDRVMTVSFHKF-GDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMGK 255
                                                                                                                                                                                                                                                                                                                                                  DDYVSFLRSITPETQQDQIR-QLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHGL 136
                                                                                                                                                                                                                                                                                                                                                                                          RVSYHFNSKVSHYHYGVKHPMKPFRLMLTDHLVSSYGLHKIMDLYETRSATRDELLQFHS 86
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                                                                                                                                                                                                                  SDIAINWSGGLHHAKKNSPSGFCYVNDIVLSILNLLRYHPRILYIDIDLHHGDGVQEAFY
                                                                                                                                                                                                                                                                                                     EDYVNFLSKVSPENANKLPRGTLENFNIGDDCPIFQNLYDYTTLYTGASLDATRKLINNQ 146
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D70388
A; Reference number: S54059
A; Accession: S54089
A; Molecule type: DNA
A; Residues: 1~470 <BAD>
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A; Residues: 1-375 < AQF>
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                                                                                                         R; Badcock, K.;
                                                                                                                           C; Accession: S54089
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mes 116; Conserv
                                                                                                                                                                                                                                                                                                                         PYALARAWTLIWCELSGREVPEKL-
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                                                                                                         Churcher, C.M
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                                                                                Library,
                                                                                  May 1995
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hypothetical protein YPR068c - yeast (Saccharomyces cerevisiae) N;Alternate names: hypothetical protein YP9499.23c C;Species: Saccharomyces cerevisiae
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C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 31-Mar-2000
C;Date: 08-Jul-1995 #sequence_revision 19-Oct-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE000719; NID:g2983517; PIDN:AAC07100.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VFVLSLHQSPEYAFPFEKGFLEEIGEGKGKGYNLNIPLPKGLNDNEFLFALEKSLEIVKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VMTVSFHKFGDY-FP-GTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMGKVME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.5%; Score 475; DB 2; 32.4%; Pred. No. 3.9e-29; tive 67; Mismatches 127
                                                                                                                                                                                                                                                                                                                                                                                                                               ---NVAFLKAFNIVREVFGEGVYLGGGGYH
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   #text_change 06-Feb-1998
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A;Cross-references: EMBL:Z49219; NID:g805025; PID:g805048; MIPS:YPR068c A;Experimental source: strain AB972 C;Genetics: Ş Q 밁 γ Db Ş Дb QY Вþ δÃ A:Cross-references: SGD:SO006272; MIPS:YPR068c A:Map position: 16R C:Superfamily: RPD3/acuC homology F:9-383/Domain: RPD3/acuC homology <RAH1> Db Q В 밁 A; Gene: SGD: HOS1 Query Match 17.3%; Score 471.5; DB 2; Length 470; Best Local Similarity 28.6%; Pred. No. 9.9e-29; Matches 128; Conservative 65; Mismatches 133; Indels 121; Gaps 436 YOYWIY----EMEGSSRMKML---RND 455 140 INNSEVPTNDKPTDTYILNSETKQYNLEGDCPIESYLPMYCQVITGATLNLLDHLSPTER 199 316 PLIERHEPEALIIECGGDGLLGDRFNEWQLTIRGLSRIIINIMKSYPRAHIFLLGGGGYN 375 349 --YTLHVAPSNMENKNSROMLEEIRND 373 376 DILMSRFYTYLTWCVTKQFSNLRCGDNNSFQIDPFDVCDGDDSEQFIREHDLVEMYNEEN 435 313 IRNVARCWCYET------348 255 KVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAE-CVKFMRSF-NVPLLLLGGGGYT 312 260 YSKQIQTISVHLYEPGFFPGTGSLSD----SRKDKNVVNIPLKHGCDDNYLELIASKIVN 315 197 ATDRVMTVSFHKF-GDYFPGTGHIQDIGYGSGKYYS-LNVPLDDGIDDESYHLLFKPIMG 254 96 85 37 PMKPH-RIRMTHALLAHYGLLQHMQVLKPFP-ARERDLCRFHADDYVSFL------ 84 80 QDVNNPMVESKWSELSELADNWNEKIDYNPSQDLQRFTTRENLYNYYLNHSQALENNMDC 139 20 PCNNHQKSQLTYSLINAYDLLQHFDEVLTFPYARKDDLLEFHSKSYIDYLINGRFNKMMA 79 95 IR------QLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHGLC 137 14;

Search completed: April 26, 2002, 17:52:45 Job time: 108 sec

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US-09-282-305-8
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US-09-282-305-1
US-08-717-365-1
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US-09-282-305-4
US-09-282-305-1
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US-09-284-564A-2
US-08-568-459A-4
US-08-868-459A-4
US-07-814-964-11
US-08-288-442-11
US-08-288-442-11
US-08-28-440-5
US-08-630-349-5
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242 DESYHLLFKPIMGKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGH	3 TGGNSLAS-GPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALI 3 ITTT	TT 1 9-282-305-8 quence 8, Application US/09282305 tent No. 6287943 tent No. 6287943 NERAL INFORMATION: Donald A. PPLICANT: Baldwin, Donald A. PPLICANT: Briggs, Steven P. PPLICANT: Grane, Virginia C. ITLE OF INVENTION: Maize Histone Deacetylases And TILE REFERENCE: 5718-44, URRENT APPLICATION NUMBER: US/09/282,305 URRENT FILING DATE: 1999-03-31 RIOR FILING DATE: 1998-04-03 RIOR FILING DATE: 1998-04-03 UNBER OF SEQ ID NOS: 18 OFTWARE: Patentin Ver. 2.0 Q ID NO 8 OFTWARE: Patentin Ver. 2.0 TYPE: PRT ORGANISM: Zea mays 9-282-305-8 9-282-305-8 9-282-305-8 9-282-305-8 9-282-305-8 9-282-305-8 9-282-305-8 9-282-305-8 9-282-305-8 9-282-305-8 9-282-305-8 9-282-305-8 9-282-305-8	28 88.5 3.3 1456 1 US-08-803-972-2 29 88.5 3.3 3052 2 US-08-557-122A-26 30 88 3.2 262 1 US-08-106-981-6 31 88 3.2 411 2 US-08-741-134-6 32 87.5 3.2 258 4 US-08-961-083-90 33 87.5 3.2 258 4 US-08-961-083-218 34 87 3.2 1388 2 US-08-760-745-5 36 86.5 3.2 237 2 US-08-760-745-5 37 86.5 3.2 255 4 US-09-760-745-5 38 86.5 3.2 764 1 US-09-177-431-4 40 86.5 3.2 764 1 US-09-177-431-4 41 86.5 3.2 1089 1 US-08-780-7431-2 42 86.5 3.2 1089 3 US-09-177-431-2 43 86.5 3.2 1089 1 US-08-750-2 44 86 3.2 254 2 US-08-75-300-2 45 86 3.2 554 3 US-09-177-431-2 46 86 3.2 554 3 US-09-052-778-16
EKGHAECVKFMRSFNV 301	THALLAHYGLLOHMQV 61	heir Uses Length 517; Length 517;	Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 90, Appli Sequence 218, Appli Sequence 4, Appli Sequence 5, Appli Sequence 6, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 2, Appli

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LENGTH: 439
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CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Malze Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         68 RPHPARDRDLCRFHADDYVSFLRSVTPETQQDQIRALKRFNVGEDCPVFDGLYSFCQTYA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSRQMLEEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDSDMDVD 421
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                                                                        TRHQLDDIKSKLLDNLSKLRHAPSVQFQERPPEAELPEQUEDKENPDERHDADSDVEM-N
                                                                                                        SROMLEEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDSDMDVDD 422
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US-08-528-255A-1

Sequence 1, Application US/08528255A Patent No. 5659016 GENERAL INFORMATION:

APPLICANT: NAKAMURA, YUSUKE
APPLICANT: : FURUKAWA, YOICHI
TITLE OF INVENTION: RPDL PROTEIN
TITLE OF INVENTION: ENCODING THE

NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:

ADDRESSEE:

THIEL,

BOUTELL & TANIS,

P.C

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GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And
FILE REFERENCE: 5718-44,
CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 00/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
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QRSRLWSGGAYDSDTEDPDSLK 438
                                                                                                   LEEIRNDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDSDMDVDDDRKP 426
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                                                                                                                                                                                            GGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQM 366
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                                                                             LENIKNMILENLSKIEHVPSTQFHDRPSDPEAPE -- EKEEDMDK---
                                                                                                                                                        GGGGYTIRNVARCWCYETAVAVGVEPDNKLPYNDYYEYFGPDYTLHIQPKSVENLNTTKD 371
                                                                                                                                                                                                                                                                                                                  {\tt HGDGVEEAFFTINRVMTVSFHKYGDFFPGTGHITDVGAAEGKHYALNVPLSDGIDDTTFR}
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63,3%;
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2026 Rambling Road

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US-08-528-255A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: JP6-227876
FILING DATE: 22-SEPTEMBER-1994
APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: human
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: Furuya Case 1335 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134
419 DVDDDRKPIPS-----RVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTKVTGVNP 473
                                            366 LFENLRMLPHAPGVQMQAIPEDAIPEESGDEDEDDPDKRISICSSDKRIACEEEFSDSEE
                                                                                                                                                                                     314 RNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEEIRND 373
                                                                                                                                                                                                                                         246
                                                                                                                                                                                                                                                                                254 GKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTI 313
                                                                                                                                                                                                                                                                                                                                    186
                                                                                                                                                                                                                                                                                                                                                             194 AFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIM 253
                                                                                                                                                                                                                                                                                                                                                                                                                             126 KQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGVEE 185
                                                                                          374 LLHNLSKLQHAPSVPFQERPPDTETPEV-DEDQEDGDKRWD---
                                                                                                                                         306 RNVARCRTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIKQR 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 GYKRKYCYFYDPEYGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQYLKPFPARERDLC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Terryence F. Chapman REGISTRATION NUMBER: 32549
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CITY: Kalamazoo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 RFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLN 133
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                                                                                                                                                                                                                                       SKVMEMFQPSAVVLQCGSDSLSGDRLGCFNLTIKGHAKCVEFVKSFNLPMLMLGGGGGYTI 305
                                                                                                                                                                                                                                                                                                                                    AFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAIFKPVM 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KYHSDDYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMT 65
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Pred. No. 6.8e-154;
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Patent No. 5763182
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: FURUKAWA, YOIG
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage

COMPUTER: IBM PC/XT/AT Compatible
                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens IMMEDIATE SOURCE:
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NAME: Terryence F. Chapma
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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FILING DATE: September 14, 1999
APPLICATION NUMBER: JP6-227876
FILING DATE: 22-SEPTEMBER:1994
APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY-1995
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CITY: Kalamazoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Terryence F. Chapman REGISTRATION NUMBER: 32549
                                  74 REHADDYVSFLRSITPETQQDQIRQLKRENVGEDCPVFDGLYSFCQTYAGGSVGGSVKLN 133
                                                                                                                                                                      Match 56.2%; Score 1530; DB 1; Local Similarity 59.2%; Pred. No. 6.8e-154;
                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/717, 365
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66 KYHSDDYIKFLRSIRPDNMSEYSKQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVKLN 125
                                                                                                              14 GVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLC 73
                                                                                                                                                                                                                                                                         LIBRARY:
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                                                                          6 GTRRKVCYYYDGDVGNYYYGQGHPMKPHRIRWTHNLLLNYGLYRKMEIYRPHKANAEEMT 65
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UMBER: JP6-227876
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CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 432
                                                                                                                                                                                                                                                                                                                  Query Match 50.0%; Score 1360; DB 4; Length 432; Best Local Similarity 59.0%; Pred. No. 6.8e-136; Matches 249; Conservative 61; Mismatches 92; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09282305 Patent No. 6287843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C.
                  198 TDRVMTVSFHKFGD-YFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIMGKV 256
                                                                                                138 DIAINWAGGLHHAKKCEASGECYVNDIVLAILELLKQHERVLYVDIDIHHGDGVEEAFYA 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
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                                                                                                                                                                                                                                                             21 YFYDP---EVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLCRFHA 77
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                                                                                                                                                        ADYVEFLHRITPDSQHLYASELTRYNLGEDCPYFDNLFEFCQIYAGGTLDAARRLNHKIC 127
TDRVMTVSFHKYGDLFFPGTGDIKDIGEREGKYYAINIPLKDGIDDTSFTRPFKTIIAKV 247
                                                                              DIAINWAGGLHHAKKCEASGFCYINDLYLGILELLKYHARVLYIDIDVHHGDGVEEAFYF 187
                                                                                                                                                                                                                                      YFITPIVGDVGNVYFGPNHPMKPHRLCMTHHLVLSYGLHQKMEIYRPHKAYPIELAQFHS 67
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                                                                                                                                                                                                 DDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVKLNHGLC 137
                                                                                                                                                                                                                                                                                                                    Indels 20;
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309	265 LENIKUMILENLSKIJHAPSVYFQERVEDIEITEVDELVEDGURRMDYDDDRAF 	B 4
0 0	07 GGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSROM +	Db Qy
306 204		Db Qy
246 144	187 HGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYH 	P 94
186 84	127 GGSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIH	Db Qy
45	46	Дb
126	67 ARERDLCRYHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSV	Qy
66 45	7 SLASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFP ; ; ; : ; 12 SPAGGEDAHRRRVSYFYEPSIGDYYYGQGHPMKP	Оy
ps	Query Match 41.5%; Score 1130.5; DB 4; Length 351; Best Local Similarity 48.9%; Pred. No. 1.2e-111; Matches 216; Conservative 50; Mismatches 53; Indels 123; Ga	7 m 0
	SSULT 7 5-09-282-305-4 5-09-282-305-4 5-09-282-305-4 5-09-282-305-4 FACTORIC BARRATION US/09282305 SEQUENCE 4, Application US/09282305 SEQUENCE 1 INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44, CURRENT FILING DATE: 1990-03-31 PRIOR APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1990-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 351 TYPE: PRT ORGANISM: Zea mays 5-09-282-305-4	US-S-S-S-S-S-S-S-S-S-S-S-S-S-S-S-S-S-S-
	421 DD 422 	Db Qy
420 427	377 NLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKR	Оy
376 367	317 ARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSROMLEEIRNDLLH : ::: ::	D Qy
316 307	257 MEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGYTIRNV : : :	Qy Db

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IPSRV-KREAVEPDTKDKDGLK 447

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310 QRSRLWSGGAYDSDTEDPDSLK 331

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US-09-214-564A-2

: Sequence 2, Application US/09214564A

: Patent No. 6150315
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GENERAL INFORMATION:
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Patent No. 6218150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/446,504
CURRENT FILLING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: FUJITA, Tomoko
APPLICANT: MUYAKE, Kazue
APPLICANT: MUKAI, Hiroyuki
APPLICANT: ASADA, Kiyozo
APPLICANT: KATO, Ikunoshin
TITLE OF INVENTION: DNA POLYMERASE-RELATED
FILE REFERENCE: 1422-408ECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: JP 9
PRIOR FILING DATE: 1997-06-5
PRIOR APPLICATION NUMBER: JP 9
PRIOR FILING DATE: 1997-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: UEMORI, Takas
APPLICANT: SATO, Yoshimi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                             327 DIL 329
                                                                                                                                                                                    372 NDL 374
                                                                                                                                                                                                                           293 DKGFPAFIMGYEEGKA-----KAREEPRYE----TLKLA--
                                                                                                                                                                                                                                                                                                            233 LPIVEEVKPKVIVISAGFDGFKGDGLTTLRLTESFYSYAGATLNKYPLAFILEGGYGVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 LYRPPGHHAGRRGRAMGAPTLGFCIFNNAASAYVTLKEEGYGKVYVIDFDAHHGNGTQEI 174
                                                                                                                                                                                                                                                                                                                                                   254 GKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGGYTI 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 INWAGGLHHAKKCEAS···--GECYVNDIVLAILELLKQH-ERVLYVDIDIHHGDGVEEA 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 24.2 hes 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 NFVK----EAVEKGITRL-----DPDTYVSPGTWSAALLALGAARSAALSALHYGGLHMA 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 SFLRSITPETOQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGSVK-LNHGLCDIA 140
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                                                                                                                                                                                                                                                        RN--VARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEEIR 371
                                                                                                                                                                                                                                                                                                                                                                                               FWNDPDVIHIDLHE-RDIYPGSGDVSEVG-GSNAYGSKINLPMPHYSGDGDYIYVWDEIV
                                                                                                                                                                                                                                                                                                                                                                                                                                    FYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYS-LNVPLDDGIDDESYHLLFKPIM 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FYSKKFNLHRPSEYHPENPKRLEIVLSKVRELGLEERIE--EPNPVEETFVEKIHDRDYI 63
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24.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 253.5; DB 4
Pred. No. 2.1e-18;
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; SOFTWARE: FASTSEQ for Wi
SEQ ID NO 2
; LENGTH: 754
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-214-564A-2
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CURRENT FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: US 60/021,218
PRIOR FILING DATE: 1996-07-03
PRIOR APPLICATION NUMBER: US 60/033,152
PRIOR FILING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: PCT/US97/11713
PRIOR APPLICATION NUMBER: PCT/US97/11713
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 5
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                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08760745 Patent No. 5972658
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT: Zhou, Qiang
TITLE OF INVENTION: TAT-SF: Cofactor For Stimulation Of Transcriptional
TITLE OF INVENTION: Elongation By HIV-1 TAT
FILE REFERENCE: M0656/7042
                                                                                                                                                 APPLICANT: Bandman, Olga
APPLICANT: Goli, Surya K.
APPLICANT: Murry, Lynn E.
TITLE OF INVENTION: LUNG GROWTH FACTOR VARIANT
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
                                                                                                     ADDRESSEE: INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 ---- RGFEGSCSQKESEEGNPVRGSEEDSPKK 500
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                                                              STREET: 3174 PO:
CITY: Palo Alto
STATE: CA
                                      COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----NLSI-----KGHAECVKFMRSFNVPLLLLGGGGYTIRNVARCWCYETGV 326
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                                                                                                                                       INCYTE PHARMACEUTICALS,
                                                                                                            Porter Drive
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                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                            APPLICANT: Sim,
APPLICANT: Chitnis, Cheunapplicant: Miller, Louis H.

Trant: Miller, Louis H.

Tharson, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEORMATION FOR SEQ ID NO:
                                                                                                                                    APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Weilems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERVTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: General Services 598956
        STATE: Newport Beach
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 469 TGVNPVGVEEASVKMEEEGTNK 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147 EKNEKGALKRRAGDLLEDSPKRPK-EAENPEGEEKEAATLEVERPLPMEVEKNSTPSEPG 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           372 NDLLHNLSKLQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDSDMD------VDDDRK 425
                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 NNPTVKASGYQSSQKKSCVEEP----EPEPEAAEGDGDKKGNAEGSSDEEGKLVIDEPAK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31 DEMPEAAVKSTANKYQVFFFGTHETAFLGPKDLFPYEESKEKFGKPNKRKGFSEGLWEIE 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 3.9%; Score 105; DB 2;
Local Similarity 23.8%; Pred. No. 0.0075;
hes 48; Conservative 27; Mismatches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US
FILING DATE: Herewith
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COMPUTER: I
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                                                                                              ADDRESSEE:
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92660
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                                                                          E: Knobbe Martens Olson & Bear
620 Newport Center Drive 16th
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                                                                              16th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77;
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Best Local Similarity
"hehes 76; Conserve
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                                                                                                                                                                                     US-08-487-826B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                           Sequence 4, Application US/08487826B Patent No. 5993827
                                                                                                                          GENERAL INFORMATION:
                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: pi
HYPOTHETICAL: NO
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                                       APPLICANT:
                                                           APPLICANT:
APPLICANT:
                 APPLICANT:
                                                                                                                                                                                                                                                                        835 IGSSPNDNINVTEQGD-NISGVNSKPLSDDVRPDKKELEDQNSDESEE 881
                                                                                                                                                                                                                                                                                                                  450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 NVARCWCYETGVALGVEVEDKMPEHEYYEY-FGPDYTLH-----VAPSNMENKNSR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509 LLMIKEH----ILAIAIYESRILKRKYKNKDDKEVCKIINKTFADIRDIIGGTDYWNDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release
                                                                                                                                                                                                                                                                                                                                                                                                                                          721 LNFEDEFKEELHSDYKNKCTMCPEVKDVPISIIRNNEQTSQEAVPEENTEIAHRTETPSI 780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                               MERGKGCEVEVDESGSTKVTGVN--PVGVEEASVKMEEEGTNKGGAEQ 495
                                                                                                                                                                                                                                                                                                                                                         SEGPK-GNEQKERD-----DDSLSKISVSPENSRPETDAKDTSNLLKLKGDVDISMPKAV
                                                                                                                                                                                                                                                                                                                                                                                                DEDQEDGDKRWDPDSDMDVDDDRKPIPSRVKREAVEPDTKDKDGL------KGI 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKSKCNSYKEWISKKKEEYNKQAK-QYQEYQKGNNYKMYSEFKSIKPEVYLKKYSEKCSN 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRKLYGKINTNSKYVHRNKKNDKLFRDEWWKVIKKDVWNVISWVFKDKTV---CKEUDIE 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----QMLEEIRNDLLHNLSKLQHAPSVPF-------QERPPD-----TETPEV 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1435 amino acids
                                                           Chitnis, Chetan
Miller, Louis H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                       Peterson, David S.
                                                                                                  Sim, Kim L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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                 Xin-zhaun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.5%; Score 96; DB 2; Length 1435;
18.6%; Pred. No. 1.4;
ative 61; Mismatches 155; Indels 116; Gaps
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HYPOTHETICAL: N
ORIGINAL SOURCE:
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LENGTH: 1435 amino acids
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REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
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NAME: Israelsen, ned
REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Rela
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TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                          315
                                                                                                                                                                                                                                                                                                                                                                                             276
                                                                                                                                                                                                                                                                                                                                                                                                                                  565 NRKLYGKINTNSKYVHRNKKNDKLFRDEWWKVIKKDVWNVISWVFKDKTV---CKEDDIE 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        509 LLMIKEH----ILATATYESRILKRKYKNKDDKEVCKIINKTFADIRDIIGGTDYWNDLS 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169 LELLKQHERVLYVDIDIHHGDGVEEAFYATD-----RVMTVSFHKFGDYFPGTGHIQDIG 223
  835
                                        450 MERGKGCEVEVDESGSTKVTGVN--PVGVEEASVKMEEEGTNKGGAEQ 495
                                                                                                                                                                       721 LNFEDEFKEELHSDYKNKCTMCPEVKDVPISIIRNNEQTSQEAVPEENTEIAHRTETPSI 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 -----YGSGKYYSLNVPLDDGIDDESYHLLFKPIMGKVMEIFRPGAVVLQCGADSLS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/487,826B FILING DATE: 10-SEP-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                              DEDQEDGDKRWDPDSDMDVDDDRKPIPSRVKREAVEPDTKDKDGL-----KGI 449
                                                                                                                                                                                                                                                             CKSKCNSYKEWISKKKEEYNKQAK-QYQEYQKGNNYKMYSEFKSIKPEVYLKKYSEKCSN 720
IGSSPNDNINVTEQGD-NISGVNSKPLSDDVRPDKKELEDQNSDESEE 881
                                                                                                                                                                                                                  ----QMLEEIRNDLLHNLSKLQHAPSVPF------
                                                                                                                                                                                                                                                                                                     NVARCWCYETGVALGVEVEDKMPEHEYYEY-FGPDYTLH-----VAPSNMENKNSR----
                                                                                                                                                                                                                                                                                                                                                                                         GDRLGCFNLSIKGHAECVKFMRSFNVPLLLLGGGGY-----TIR------
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PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                              -NIPQFFRWFSE-----WGDDYCQDKTKMIETLKVECKEKPCEDDN 661
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                                                                                   -DDSLSKISVSPENSRPETDAKDTSNLLKLKGDVDISMPKAV 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61; Mismatches 155; Indels 116; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version
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RESULT 13

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: NAME/KEY: Domain

: LOCATION: 657..72:

: OTHER INFORMATION:

US-07-814-964-11
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Patent No. 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Donahu
                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MIT-4787AAA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
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MEDIUM TYPE: Floppy disk
                                                              FEATURE:
                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                                                                                        NAME/KEY: Domain LOCATION: 518..547 OTHER INFORMATION:
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TELEPHONE: 61/-00-
TELEPHONE: 617-861-9540
TELEPHONE: 617-861-9540
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
                                                                           NAME/KEY: Domain LOCATION: 632..649 OTHER INFORMATION:
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LOCATION: 458..507
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                                                                                                                                           OTHER INFORMATION:
                                                                                                                                                              LOCATION:
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Toney, Jeffrey |
Bruhn, Suzanne
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657..723
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547..620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Essigmann, John M.
APPLICANT: Lippard, Stephen J.
TITLE OF INVENTION: DNA Structure Specific Recognition
TITLE OF INVENTION: Protein and Uses Therefor
NUMBER OF SEQUENCES: 13
                  FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
                                                                                                                                                                                                                                                                                                      ZIP: 02173
COMPUTER READABLE FORM:
                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/539,906
FILING DATE: 18-JUN-1990
                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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REGISTRATION NUMBER:
                                                                                                                                  CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                   STATE: MA
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Toney, Jeffrey H.
Bruhn, Suzanne L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: MI TELECOMMUNICATION INFORMATION: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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LOCATION:
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LOCATION: 632..64
OTHER INFORMATION:
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LOCATION: 458..5
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                                                                   T---RESIKRENPGIKVTEIAKKGG 590
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                                                                                                                                      DGAKKKKEKKSEKKEKKEKKHKEK-----ERTKKPSKKKKDSGKPKRATTAFMLWLNU 568
                                                                                                                                                                     ----RKPIPSRVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTK-----VTGVNP 473
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547..6
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657..72
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US/08328809

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LOCATION: 657..723;
COTHER INFORMATION: /1
US-08-328-809-6
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GENERAL INFORMATION:
Query Match 3.5%; Score 94.5; DB 1; Best Local Similarity 20.8%; Pred. No. 0.63; Matches 80; Conservative 38; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-248-7100 (NFORMATION FOR SEQ ID NO: 6:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Fenton, Gillian M.
REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: MIT-023 (5473/24)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Kellett, Patti
TITLE OF INVENTION: Uses For DNA Structure-Specific
TITLE OF INVENTION: Recognition Proteins
NUMBER OF SEQUENCES: 8
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ORIGINAL SOURCE:
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IMMEDIATE SOURCE:
CLONE: Drosoph
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                                                                                                                                                                            NAME/KEY: Domain LOCATION: 632..649 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                    NAME/KEY: Domain LOCATION: 518..547 OTHER INFORMATION:
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ZIP: 02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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LOCATION: 458..507
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Toney, Jeffrey H.
Bruhn, Suzanne L.
Pil, Pieter M.
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Lippard, Stephen J.
Essigmann, John M.
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T---RESIKRENPGIKVTEIAKKGG
                            VGVEEASVKMEEEG----TNKGG 492
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Search completed: Job time: 32 sec April 26, 2002, 17:51:24

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Result
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Maximum Match 10
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Copyright (c) 1993 - 2000 Comp
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Arabidopsis thalia	AAG07247	21	377		327.5	42
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S	AAG51590	21	552	2	328.5	40
ţ,	AAG51591	21	499	2	328.5	39
is	AAG51592	21	468	12.1	328.5	38
j.	AAG07246	21	398	2	333.5	37
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cys77Ser	AAU00241	22	375	7.	477	ω
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Human polypeptide	AAM42160	22	296	0.	566.5	30
Ď.	AAB70496	22	180	w	629	29
acid sequen	AAB84361	22	377	1.	852	28
	AAY83027	21	377	1.	852	27
polypep	AAM40374	22	415	1.	855.5	26
e histone	AAY28798	20	351	:	1130.5	25
histone	AAB67166	22	433	9.	1341	24
histone	AAY28801	20	432	0.	1360	23
Human histone deac	AAB49956	22	428	0	1373	22
	AAG39374	21	425	0	1382.5	21
Arabidopsis thalia	AAG05189	21	425	0		20
=	AAU00243	22	370	1.	1412	19
thali	AAG39373	21	432	2	1421.5	18
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histone	AAB49955	22	488		1494	16
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histone dea	AAB49954	22	482		S	<u>1</u> 3
Human histone deac	AAB67164	22	482	6	5	12

ALIGNMENTS

RESULT AAB67811

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AAB67811;

AAB67811 standard;

Protein;

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Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotylelongation), comprises introducing genes encoding histone deacetylase CA2316036-A1. Histone deacetylase; AtRPD3A; RPD3; gene expression; transgenic plant; HDA1; ethylene-responsive phenotype; hypocotyl elongation. N-PSDB; Miki B, 24-AUG-2000; 2000CA-2316036. Arabidopsis thaliana Amino acid sequence of a histone deacetylase designated AtRPD3A 29-JUN-2001 (first entry) (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA 27-FEB-2001. 2001-258457/27. DB; AAF80350. Brown D, 99US-0383971. Tian Ļ Ę <u>~</u>

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                   Arabidopsis histone
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                    expression;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              501 AA;
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                    disease
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3.7e-275;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a method of suppressing the expression of a gene of interest by introducing into the cell a protein containing a DNA binding site and a chromatin inactivation portion, or a nucleotide encoding such a peptide. Preferably the chromatin inactivation portion is part of the histone deacetylation (HDAC) complex. The method can be used in disease treatment, for example in the treatment of cancer by the suppression of oncogenes, and in the production of disease models.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Suppressing expression of selected gene for treating cancer, involves introducing peptide comprising nucleic acid binding portion that binds to or associated with selected gene and chromatin inactivation portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                             dddrkpipsrvkreavepdtkdkdglkgimergkgcevevdesgstkvtgvnpvgveeas
                                           DDDRKPIPSRYKREAVEPDIKDKDGLKGIMERGKGCEVEVDESGSTKVTGVNPVGVEEAS
                                                                                                                                                           vpilliggggytirnvarcwcyetgvalgvevedkmpeheyyeyfgpdytlhvapsnmen
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Pred. No. 3.7e-275;
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                                                                                                                                                                                                                                                                                                                                                                                         rice, soybean and wheat nucleic acid fragments encoding HD1. It also relates to the construction of a chimeric gene encoding all a portion of HD1, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of HD1 in a transformed host cell. The availability of
                                                                                                                                                                                                                                                                                                                                         nucleic acid sequences encoding (portions) of histone deacetylase proteins will facilitate studies of global transcriptional regulation in eukaryotic cells, and will also provide mechanisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HD1), a chromatin associated protein, as deduced from a soybean root cDNA clone (see AAZ58260) isolated on the basis of homology plant histone deacetylases. The invention relates to isolated
                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                              control transcriptional gene regulation in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of soybean histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 27-28; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid fragment useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-1998;
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                                                                                                                                                                       1 MDTGGNSLASGPDGVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQ 60
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VDIDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGI 240
                                           YAGGSYGGSYKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLY 180
                                                                                           vlkpmaakdrdlckfhaddyvaflrgitpetqqdqlrqlkrfnvgedcpvfdglysfcqt 120
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80.7%;
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Pred. No. 3.5e-214;
3; Mismatches 37;
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The present sequence is maize histone deacetylase encoded by HD cDNA belonging to family 1, ZmHD1. This enzyme responsible for removing acetyl modifications, may be localised to promoters targeted for repression by other proteins that associate with HD and specifically bind regulatory elements in promoter DNA. The HD nucleotide sequence can be used for producing transgenic plants with increased disease resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maize histone deacetylase; HD; HD cDNA; family 1, ZmHD1; gene repression; acetyl modification; promoter; regulatory element; transgenic plant; disease resistance; toxin screening; pathogenicity;
                                       Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are
                                                                                                                                                                  Claim 1; Page 63-65; 87pp; English.
                                                                                                                                                                                                                                                                                  Baldwin DA,
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                                                                                                                                                                                              New deacetylase genes, used for producing transgenic plants which have increased disease resistance \,
                                                                                                                                                                                                                                                                                                                                                                    02-APR-1999;
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                           by histone deacetylase
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Sequence

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              New nucleic acid fragment useful as probes and
                                         N-PSDB; AAZ58259
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                                                                                                                                                                                                                                                                                              Chromatin associated protein; histone deacetylase gene 1; HD1;
                                                                                                                                                                                                                                                                                                                        Rice histone deacetylase 1 (HD1) protein (C-terminal portion).
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                                                         2000-182439/16.
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                                                                                   Vollmer
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RESULT AAY28799 ID AAY2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA libraries on the basis of homology to other plant histone deacetylases. The invention relates to isolated rice, soybean and wheat nucleic acid fragments encoding HD1. It also relates to the construction of a chimeric gene encoding all or a portion of HD1, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of HD1 in a transformed host cell. The availability of nucleic acid sequences encoding (portions) of histone deacetylase proteins will facilitate studies of global transcriptional regulation in eukaryotic cells, and will also provide mechanisms to control transcriptional gene regulation in plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of a C-terminal portion of rice histone deacetylase 1 (HD1), a chromatin associated protein, as deduced from a cDNA contig (see ARX58259) obtained from CDNA clones isolated from rice callus, 15-day-old leaf and 15-day-old seedling
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                                                    LQHAPSVPFQERPPDTETPEVDEDQEDGDKRWDPDSDMDVDDDRKPIPS------R 430
                                                                                                                                                                                                                                                                          RPGAVVLQCGADSLSGDRLGCENLSIKGHAECVKFMRSENVPLLLLGGGGYTIRNVARCW 320
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                                                                                               VKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTK---VTGVNPVGVEE-ASVKMEEE 486
                                                                                                                                                                                            cyetgvalgheltdkmppneyfeyfgpdytlhvapsnmenkntrqqlddirsrlldnlsk 359
                                                                                                                                                                                                                              CYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKNSRQMLEEIRNDLLHNLSK 380
                                                                                                                             lrhapsvqfqerppeaelpeqdedqedpderhhadsdvem-ddvkplddsgrrssiqnvr 418
                                                                                                                                                                                                                                                              rpgavvlqcgadslsgdrlgcfnlsirghaecvrfmrsfnvpllllqqqqytirnvarcw
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78.1%;
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Pred. No. 2.9e-200;
6; Mismatches 54;
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                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-611038/52.
N-PSDB; AAX90839.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
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                                                                    LLLLGGGGYTIRNVARCWCYETGVALGVEVEDKMPEHEYYEYFGPDYTLHVAPSNMENKN
                                                                                                                                                               IDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDD
                                                                                                                                                                                                                                           {\tt rphpardrdlcrfhaddyvsflrsvtpetqqdqlralkrfnvgedcpvfdglysfcqtya}
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             trhqlddikskildnlsklrhapsvqfqerppeaelpeqdedkenpderhdadsdvem-n
                                                        {\tt llllggggytirnvarcwcyetgvalgheltdkmppneyyeyfgpdytlhvapsnmenkn}
                                                                                                                                                  {	t idihhgdgveea} {	t fyttdrvmtvsfhkfgdyfpgtgdirdvghskgkyyslnvplddgidd}
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58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease resistance
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84.2%;
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Pred. No. 1.2e-194;
99; Mismatches 35;
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                            Arabidopsis thaliana
                                          Histone deacetylase; AtRPD3B; RPD3; gene expression: transgenic HDA1; ethylene-responsive phenotype; hypocotyl elongation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents Arabidopsis thaliana histone deacetylase designated AtRPD3B. The protein is homologous to yeast RPD3 and HDA1. The polynucleotide sequence is used in the method of the invention. The specification describes a method for regulating gene expression in transgenic plants. The method comprises modifying histones by introducing chimeric nucleotide sequences which have regulatory elements in operative association with a gene of interest or with a nucleotide sequence encoding histone deacetylase. The method is useful for regulating the developmental, physiological or biochemical pathway within a plant,
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AAY28797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is maize histone deacetylase encoded by HD cDNA belonging to family 1, ZmHDI. This enzyme responsible for removing acet modifications, may be localised to promoters targeted for repression by other proteins that associate with HD and specifically bind regulatory elements in promoter DNA. The HD nucleotide sequence can be used for producing transgenic plants with increased disease resistance. Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maize histone deacetylase; HD; HD cDNA; family 1, ZmHD1; gene repression; acetyl modification; promoter; regulatory element; transgenic plant; disease resistance; toxin screening; pathogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-611038/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-OCT-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease response promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maize histone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New deacetylase genes, used for producing transgenic plants which have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9951731-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                increased disease resistance
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HGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYH
                                                                                                                                                                                                                                                                    p 462
                                                                       aseadirrfhsddyvaflasatgnpgvldpraikrfnvgedcpvfdglfpfcgasaggsi 131
                                                                                                                     GGSVKLNHGLCDIAINWAGGLHHAKKCEASGFCYVNDIVLAILELLKQHERVLYVDIDIH 186
                                                                                                                                                                                                                         ARERDLCRFHADDYVSFLRSITPETQQDQIRQLKRFNVGEDCPVFDGLYSFCQTYAGGSV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Page 49-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by histone deacetylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   458
                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             Score 1548; DB 20;
Pred. No. 1.4e-152;
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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influencing cell cycle progression or to modulate gene transcription. The products can be used for diagnosis and therapy. They can be used, for example, to treat tumours or proliferative disorders or spermatogenesis, osteogenesis, chondrogenesis or the differentiation of progenitor cells. They can also be used to treat psoriasis, bone diseases, fibroproliferative disorders, degenerative disorders, or for repair of cartilage, increasing bone density, liver repair subsequent to a partial hepatectomy, to promote regeneration of lung tissue in the treatment of emphysema, or for inducing tolerance in autoimmune diseases, and transplant recipients. Hox inhibitors can be used as anti-fungal agents, preservatives in foodstuff, feed supplements for promoting weight gain in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Histone deacetylase gene; HDx; HDl; HDx polypeptide; H4; cell differentiation; chromatin structure; cell oppoliterative disorder; fibroproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                   proteins are able to alter chromatin structure by deacetylating histones such as H3 or H4. They have the ability to modulate cell growth by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide, designated HD1. The HDx polypeptides are capable of modulating proliferation survival and differentiation of cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a novel histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Pages 112-114; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated histone deacetylase polypeptide(s) and genes develop products for modulating the proliferation, survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   degenerative disorder; autoimmune disease; HDx inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  also be used in cell cultures. note: in the claims, the full length HDl sequence is incorrectly referred to as SEQ. ID. No.2; from the disclosure it is clear that HDl is SEQ. ID. No.5.
                                                                                                                                                                Human; gene expression;
chromatin inactivation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                          28-JUN-2000; 2000WO-GB02497
                                                                                                      W0200102019-A2
                                                                                                                                                                                                            Human histone deacetylase 1 HDAC1.
                                                                                                                                                                                                                                                                                                      AAB67164 standard; Protein; 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            livestock, disinfectants, insecticides or defoliants.
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59.4%;
                                                                                                                                                             disease model; treatment; suppression; DNA binding site; histone deacetylation
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Best Local Similarity
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                    08-MAR-2001
                                                                                  AAB49954 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               essing expression of selected gene for treating cancer, involves ducing peptide comprising nucleic acid binding portion that binds associated with selected gene and chromatin inactivation portion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense oligonucleotide that inhibits expression of a histone deacetylase, useful for treating and/or alleviating the symptoms neoplasia, or for inhibiting neoplastic cell growth in an animal
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             DVDDDRKPIPS----RVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTKVTGVNP
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                                                                                                            {\tt rnvarcwtyetavaldteipnelpyndyfeyfgpdfklhispsnmtnqntneylekikqr}
                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell cycle; tumourigenesis; cancer; inhibitor; antisense;
                                                                                                                                                                                                                                                        482 AA;
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59.4%;
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Best Local
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                                                                                                                                                                                               gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the presentable.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
                                                                                                                                                                                                                                                   or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive,
                                                                                                                                                                                                                                                                                                                                  cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities,
                                                                                                                                                                                                                                                                                                                                                                 proteins, called prostate cancer antigens, given in AAB56363 to AAB57302 The prostate cancer antigens can have neuroprotective, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 2005-2006; 2338pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prostate cancer associated gene sequences, referred to cancer antigens, useful for treatment, prevention, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAR-2000; 2000WO-US05988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200055174-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human prostate cancer antigen protein sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB56985 standard; Protein;
                                                                                                                                                                                                                                                                                                     polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                     AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wound; infectious disease
                                                                                                                                                                                                                                                                                and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
(ROSE/) ROSEN C A.
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   12
                                                                                     Local Similarity
                                  14 GVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLC 73
2000-587513/55
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                                                                    Conservative
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Pred. No. 4.2e-152;
7; Mismatches 98;
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diagnosis of
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AAR88919
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   Transcription; expression; control; diagnosis; study; cancer; mammary; gastric carcinoma; chromosome 1p34.1.
AAR88919 is a transcriptional control protein, RPI human foetal lung cDNA library. The gene encoding
                                           Claim 1; Page 10-12; 15pp; English
                                                                                      New human transcriptional control protein RPDL - used to develop prods. for study and diagnosis involving the protein, partic. fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR88919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR88919 standard;
                                                                                                                                   N-PSDB; AAT12940
                                                                                                                                                                                                                                                         22-SEP-1994;
                                                                                                                                                                                                                                                                                     21-SEP-1995;
                                                                                                                                                                                                                                                                                                                    24-APR-1996
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                                                                                                                                                                               Furukawa Y, Nakamura
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   derived from a DL is localised
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       at 1p34.1 on the short arm of chromosome 1, this is a region where a deletion is recognised in mammary and gastric carcinomas. The RPDL gene is an important gene and has been found to be expressed in all the following human tissues: heart, kidney, liver, lung, pancreas, placenta, skeletal muscle, large intestine, peripheral leukocyte, ovary, prostate, small intestine, spleen, testis and thymus gland; but is not present in brain tissue. RPDL cDNA exhibits homology with the yeast transcription factor RPD3 and is believed to have a similar function. RPDL and DNA encoding it can be used in studying the interactions of the protein with DNA and other proteins in the cell.
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473 kgvke-evkl 481
                                   474 VGVEEASVKM 483
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                                                                                                           419 DVDDDRKPIPS-----RVKREAVEPDTKDKDGLKGIMERGKGCEVEVDESGSTKVTGVNP 473
                                                                                                                                                                                                                    306 rnvarcrtyetavaldteipnelpyndyfeyfgpdfkihispsnmtngntneylekikgr 365
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                                                                                                                                                                                                                                                                                            194 AFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDGIDDESYHLLFKPIM 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 GVKRKVCYFYDPEVGNYYYGQGHPMKPHRIRMTHALLAHYGLLQHMQVLKPFPARERDLC 73
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                                                                      egeggrknssnfkkakrvkte----dekekd-----peekk----
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7;

Search completed: April 26, 2002, 17:52:13 Job time: 81 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                Database :
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Perfect score:
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Maximum DB seq length: 2000000000
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 SPTREMBL_17:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fung1:*
4: sp_humao:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organe1:
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebr
14: sp_unclass
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Gapop 10.0 , Gapext 0.5
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2544
1 MEADESGISLPSGPDGRKRR.....TGEDEMDDDNPEPDVNPPSS 471
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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_fungi:*
sp_plant:*
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sp_virus:*
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sp_unclassified:*
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sp_phage:*
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sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

acore	Md LCH	тепаси	Ü	10	Description
2542	99.9	471	10	Q9FVE5	Q9fve5 arabidopsis
2535	99.6	471	10	Q9FML2	
1738	68.3	458	10	Q9ZTP8	
1560.5	61.3	501	10	Q9SZL3	-
1522	59.8	500	10	Q9LKG1	_
1496.5		493	10	Q9AXF0	_
1476		521	ن	077213	077213 drosophila
1476	58.0	521	ű	Q9VZA1	Q9vzal drosophila
1373	54.0	687	ىي	Q9P4F5	Q9p4f5 emericella
1369	53.8	409	10	Q9FH09	Q9fh09 arabidopsis
1305.5	51.3	465	υī	062339	062339 caenorhabdi
1292.5	50.8	428	11	Q99PA0	Q99pa0 rattus norv
1288	50.6	444	u	Q9GUA8	Q9gua8 cryptospori
1284	50.5	648	بى	Q9C1C6	Q9c1c6 cochliobolu
1281	50.4	449	ر.	Q9XYC7	Q9xyc7 plasmodium
1277.5	50.2	428	11	90MC60	Q9jm08 mus musculu
1275.5	50.1	428	11	Q9JL X 5	Q9jlx5 mus musculu
1275	50.1	405	w	059702	059702 schizosacch
1233.5	48.5	438	σ	Q9VNC2	Q9vnc2 drosophila
	2542 2532 2536 2536 1560.5 1738 1822 1496.5 1476 1476 1373 1369 1369 1369 1384 1288 1288 1288 1288 1288 1288 1288 12	;	99.9 471 99.6 471 68.3 458 61.3 501 58.8 493 58.0 521 54.0 682 50.8 4424 50.5 648 50.2 428 50.1 428 50.1 428 48.5 438	99.9 471 99.6 471 99.8 500 59.8 500 59.8 6493 58.0 521 58.0 687 50.1 3 469 50.2 428 50.1 428 50.1 428 50.1 428 50.1 428	99.9 471 10 99.6 471 10 68.3 458 10 58.8 501 10 58.8 493 10 58.0 521 5 58.0 521 5 54.0 687 3 54.0 409 10 51.3 465 5 51.3 465 5 51.3 465 5 50.6 444 5 50.5 648 3 50.1 428 11 50.1 428 11 50.1 428 11 50.1 428 11

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Q9utu/ homo sapien	Q91s38 arabidopsis	Q9hsp7 halobacteri	017323 caenorhabdi	Q9sje6 arabidopsis	Q9j173 mus musculu	Q9fnq7 arabidopsis	Q9xyx1 drosophila	Q91xn8 arabidopsis	067877 aquifex aeo	Q9hxml pseudomonas	Q99tc9 staphylococ	Q9k7x1 bacillus ha	Q9wx04 streptomyce	067135 aquifex aeo	Q9h368 homo sapien	K >	Q9grp1 leishmania	Q9nyh4 homo sapien	Q9np76 homo sapien	Q9d0k6 mus musculu	09p4f4 emericella	Q9qt74 tetrahymena	Q9gu59 cryptospori	Q9mln6 arabidopsis	Q9hdt2 ustilago ma

ALIGNMENTS

FCRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFK 180	QY 121 FCRASAGGSIGAAVKLNRQDADIAIN
LEISRPSLADASDIGREHSPEYVDFLASVSPESMGDPSAARNLRRENVGEDCPVFDGLED 120	Db 61 LEISRPSLADASDIGRFHSPEYVDFL
LEISRPSLADASDIGREHSPEYVDELASVSPESMGDPSAARNLRRENVGEDCPVEDGLED 120	Qy 61 LEISRPSLADASDIGRFHSPEYVDFL
MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRR 60	Db 1 MEADESGISLPSGPDGRKRRVSYFYE
MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRR 60	Qy 1 MEADESGISLPSGPDGRKRRVSYFYE
Pred. No. 5.3e-198; 0; Mismatches 0; Indels 0; Gaps	Best Local Similarity 100.0%; Power Matches 471; Conservative 0;
3543. DB 10.	90 99.
371BF7040E508849 CRC64;	SEQUENCE 471 AA; 52720 MW;
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tylse. 1.	<pre>DR</pre>
•	
BL/GenBank/DDBJ databases.	•
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istone deacetylase homologs in	
n D., Miki B.;	
sicaceae: Arabidopsis	
Spermatophyta: Magnoljophyta: endjectyledons: core endjects: Rosidae:	OC Spermatophyta: Magnoliophyta: eudicotyle
	OF PUTATIVE HISTONE DEACETYLASE.
st annotation update)	01-JUN-2001 (TrEMBLrel. 17,
Last sequence update)	16,
Created)	(TrEMBLrel. 16,
	Q9FVE5;
PRT: 471 AA.	9FVE5 PRELIMINARY;
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L DNA Res. 4:401-414(1997).
L DNA Proj. IPPO00286; BAB10553.1;
Interproj. IPPO00286; His deacetylse.
PFINTS; PF00850; Hist_deacetyl; 1.
SEQUENCE 471 AA; 52651 MM; California.
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Spermatophyta; Magnollophyta; eudlcotyledons; core eudlcots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
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01-MAR-2001
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{\tt RVLYIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPL}
                         RVLY1DTDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPL
                                                                                                                            FCRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFK
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S., Kaneko T.,
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Pred. No. 1.9e-197;
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Q9ZTP8;
Q1-MAY-1999
01-MAY-1999
01-JUN-2001
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Pipal A., Wegener S.;
Pipal A., Wegener S.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ
EMBL; AF045473; AAD10139.1; -.
Mendel; 39025; Zeama; 3043; 39025.
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Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
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Eukaryota; Viridiplantae;
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                       CLRFLRSYNVPMMVLGGGGYTIRNVARCWCYETAVAVGVEPDNKLPYNDYYEYFGPDYTL
                                  CLRFLRSYNVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTL
                                                                                                                                                             DGLFDFCRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILEL 175
                                                                                                                                                                                                                      HRRLEISRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSA--ARNLRRFNVGEDCPVF 115
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yta; Liliopsida; Poales; Poaceae; PACC cl
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Pred. No. 8.5e-133;
1; Mismatches 72;
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submitted (MAR-2000) to the EMBL/GenBs
EMBL; AL03538; CAB37533.1; -
EMBL; AL161593; CAB80478.1; -
InterPro: IPR000286; H1s_deacetylse.
Pfam; PF00850; H1s_deacetyl; ENBERGER, PF0MS50; HDASUPER.
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01-MAY-2000 (TremBLrel.
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HISTONE DEACETYLASE.
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Mayer K.F
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                         IDDESYHLLFKPIMGKVMEIFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKFMRSF
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.X., Schueller C.;
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he EMBL/GenBank/DDBJ
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64; Mismatches 94; Indels 31;
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EMBL; AF28285; AAF82385.1; -
InterPro; IPR000286; Hist_deacetylse.
Pfam; pF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
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NLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPED--DMETRPKPRXWSG
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                                                    NVPLLLVGGGGYTIRYVARCWCYETGVALGFELDDKIPQHEYYEYFGPDYTLHVAPSNME
                                                                                                  NVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPME
                                                                                                                                                            IDDESYQSLFKPIMGKVMEIFKPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVKYMISF
                                                                                                                                                                                                                                                                  YVDIDIHHGDGVEEAFYTTERVMTVSFHKFGDYFPGTETFVYIGYGKGKYYSLNVPLDDG
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61.5%;
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Best Local Similarity
Matches 294; Conserv
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermarophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, HISTONE DEACETYLASE HD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF332875; AAK01712.1; -. SEQUENCE 493 AA; 55054 MW; 0EE300BB42243Cl3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9AXFO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Song F., Goodman R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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ADDPGS
                                            VNPPSS
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                                                                                                                                              -DDDKPLHGYSCRG----GATTDRDSTGEDEMDDDN-----
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EMBL; AF086715; AAC61494.1;
FlyBase; FBgn0015805; Rpd3.
InterPro; IPR000286; His_deacetylse
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Drosophila melanogaster (Fruit fly)
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PRINTS; PR01270; HDASUPER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIGRF
                                                                                                                                                                                                                                                                                                           YSDSEDEGE------GGRRDNRSYKGQRKRPRLDKDTNSNKASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIRNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNIPLRDGMDDDAYESIFVPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQASEICINWGGGLHHAKKSEASGFCYVNDIVLGILELLKYHQRVLYIDIDVHHGDGVEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSDEYVRFLRSIRPDNMSEYN--KQMQRFNVGEDCPVFDGLYEFCQLSAGGSVAAAVKLN
                                                                                                                                                                                                                                                                                                                                                              ESDSDDDDKPLHGYSCRGGATTDRDSTGEDEMDDDNPEPDVNPPSS 471
                                                                                                                                                                                                                                                                                                                                                                                                                           LFENLRMLPHAPGVQIQAIPEDAINDESDDEDKVDKDDRLPQSDKDKRIVPE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLEQLSGLIHAPSVQFQHTP--PVNRVLDE-----PEDDMETRPKPRXWSGTATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKYMETFQPAAVVLQCGADSLTGDRLGCFNLTVKGHGKCVEFVKKYNLPFLMVGGGGYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSPEYYDFLASYSPESMGDPSAARNLRRFNYGEDCPYFDGLFDFCRASAGGSIGAAVKLN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKRVCYYYDSDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKATADEMTKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNVSRCWTYETSVALAVEIANELPYNDYFEYFGPDFKLHISPSNMTNQNTSEYLEKIKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                521 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58344 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.0%;
58.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1476; DB 5;
Pred. No. 1.8e-111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B0F6503D42A1BA32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               databases
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Codson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
RA Dorbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dorbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris M.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan p., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krapitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krapitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Krapitz S., Kulp D., Lai Z.,
RA Meikulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Meikulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskarn D.R., Pacleb J.M.,
RA Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Alliams S.M., Wolson K.A., Simpson M., Strong R., Sun E.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang S.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yells, Weinschland, C., Zhang G., Zhao Q., Zheng L.,
RA Yells, Yeh R., F., Zaerri J.S., Zhan M., Venter J., Zhao Q., Zheng L.,
RA Yells, R., Miller S., Pad J., La J., La J., La J., La J., La J., La J., 
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballow B. Been A. Barradalor T. Barrayta-Schuler D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0015805; Rpd3.
InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20196006; PubMed-10731132;
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                          198
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                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                    KRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIGRF 77
                       AFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLI
                                                                                                RQDADIAINMGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVEE 197
                                                                                                                                                                                                                        HSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVKLN 137
                                                                                                                                                                                                                                                                          KKRVCYYYDSDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKATADEMTKF 65
                                                                      KQASEICINWGGGLHHAKKSEASGFCYVNDIVLGILELLKYHQRVLYIDIDVHHGDGVEE
                                                                                                                                                                         HSDEYVRFLRSIRPDNMSEYN--KOMORFNVGEDCPVFDGLYEFCOLSAGGSVAAAVKLN 123
521 AA;
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58330 MW;
                                                                                                                                                                                                                                                                                                                                                                                                    58.0%;
                                                                                                                                                                                                                                                                                                                                                                          Score 1476; DB 5;
Pred. No. 1.8e-111;
6; Mismatches 89;
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Best Local
                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Characterization of two putative histone Aspergillus nidulans."; Biophys. Acta 1492:120-126(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9P4F5;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9P4F5
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000286; His_deacetylse
Pfam; PF00850; Hist_deacetyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Graessle S., Dangl M., Haas H., Mair Walton J.D., Loidl P., Brosch G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eurotiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Emericella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RPD3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HISTONE DEACETYLASE RPD3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF163862; AAF80489.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20461766; PubMed=11004483;
               296
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                                         VNFPLRDGIDDVSYKSIFEPVIKSVMEWYRPEAVVLQCGGDSLSGDRLGCFNLSMRGHAN
                                                                   LNVPLNDGMDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHAD
                                                                                                            LKMFKRVLYIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYA
                                                                                                                                                    DGLFEFCGISAGGSMEGAARLNRNKCDIAVNWAGGLHHAKKSEASGFCYVNDIVLGILEL
                                                                                                                                                                   DGLEDFCRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILEL
                                                                                                                                                                                                         SLYKKMEIYRAKPASKFEMTQFHTDEYIDFLSKVTPDNM--DAFAKEQSKYNVGDDCPVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YSDSEDEGE-----GGRRDNRSYKGQRKRPRLDKDTNSNKASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESDSDDDDKPLHGYSCRGGATTDRDSTGEDEMDDDNPEPDVNPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFENLRMLPHAPGVQIQAIPEDAINDESDDEDKVDKDDRLPQSDKDKRIVPE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLEQLSGLIHAPSVQFQHTP--PVNRVLDE-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNVSRCWTYETSVALAVEIANELPYNDYFEYFGPDFKLHISPSNMTNQNTSEYLEKIKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIRNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNIPLRDGMDDDAYESIFVP11
                                                                                                                                                                                                                                   HLHRRLEISRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVF
                                                                                                                                                                                                                                                                SGTSGPAGPPLDPIDLNVSGDRSKRVAYFYDSDVGNYAYVSGHPMKPHRIRMTHSLVMNY
                                                                                                                                                                                                                                                                                          SGISLPSGP-----DGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHY
                                                                                               LRFKQRVLYVDIDVHHGDGVEEAFYTTDRVMTVSFHKYGEYFPGTGELRDIGVGQGKYYA
Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     PR01270; HDASUPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nidulans (Aspergillus nidulans).
Fungi: Ascomycota; Pezizomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) (TrEMBLrel. 15,
) (TrEMBLrel. 15,
l (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                        687 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trichocomaceae;
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                54.0%;
                                                                                                                                                                                                                                                                                                                                                                                       75431 MW;
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Pred. No. 6.2e-1
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SEQUENCE
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DNA Res. 7:31-63(2000).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB023031; BAB09994.1; InterPro; IPR000286; His_deacetylse. Pfam; PF00850; Hist_deacetyl; 1. PRINTS; PR01270; HDASUPER.
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{\tt GGGGYTLPNVARCWCYETAIAVGEQLDNDLPGNDYMKYFRPDYKLHILPTNRQNLNTRLD}
                             GGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKD
                                                           HGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFR 250
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                                                                           SLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVL
                                                                                                                                                                                                                                                                  GRFHSPEYVDFLASVSPESMGD--PSAARNLRRFNVGEDC--PVFDGLFDFCRASAGGSI 130
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Pred. No. 6.2e-103;
0; Mismatches 89;
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01-AUG-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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EMBL; Z81106; CAB03240.1;
EMBL; Z81106; CAB03224.1;
EMBL; Z81108; CAB03224.1;
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Rhabditidae; Pelode:
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Pfam; PF00850; Hist_deacetyl; 1.
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RNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDP-SPMENLNTPKDMERIRN
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                                                                                   QKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYT1
                                                                                                                                AFYTTDRVMTVSFHKHGEYFPGTGDLKDVGAGSGKYYALNVPLRDGVDDVTYER1FRTIM
                                                                                                                                                                        {\tt AFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLI}
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Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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235; Conserv
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Matches 237
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Q9C1C6;
Q1-JUN-2001
01-JUN-2001
01-JUN-2001
HDC2.

Cochliobolus carbonum (Bipolaris zeicola),
Cochliobota; Fungi; Ascomycota; Pezizomycot.
Pleosporales; Pleosporaceae; Cochliobolus
NCBI_TaxID=5017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homolog).";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ EMBL; AF139991; AAG21919.1; -
InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
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                                                                                                                            HISTONE
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protein with homology to probable histone deacetylase 1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17,
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
CETYLASE 2.
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Last annotation updat
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Pred. No. 2.6e-96;
0; Mismatches 95;
                                                            Pezizomycotina;
                                                                                                                                                                                                                              PRT;
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MEDLINE-99229859; PubMed-10215020; Joshi M.B., Lin D.T., Chiang P.-H., Goldman Alkiwa M., Syin C.; "Molecular cloning and nuclear localization homologue in Plasmodium falciparum."; Mol. Biochem. Parasitol. 99:11-19(1999).
                                                                                                                                                                                                        Q9XYC7;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wegener S., Walton J.D.;
"HDC2, a histone deacetylase gene related to RPD3, from the filamentous fungus Cochliobolus carbonum.";
Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
EMBL: AF349677; AAK35180.1; -.
SEQUENCE 648 AA; 70940 MW; 242147C293D4EAD3 CRC64;
                                                                                                                                   Plasmodium falciparum
Eukaryota; Alveolata;
NCBI_TaxID=36329;
                                                                                                                                                                                                                                                                Q9XYC7
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                                                                                                 STRAIN-3D7
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                 HDAC1
                                                                                                                                                                                              HISTONE DEACETYLASE.
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Nes 246; Conserv
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Apicomplexa; Haemosporida; Plasmodium.
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86; Mismatches
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Last annotation updat
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Best Local
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GGGRAPGTRAKEHSTTHHLRRKNYDDDFFDLSDRDQSIVP
                            DDKPLHGYSCRGGATTD - - - RDSTGEDEMDDDNPEPDVNP
                                                                                          IRNTLLEQLSGLIHAPSVQFQHTPP--VNRVLDEPEDDMETRPKPRXWSGTATYESDSDD 431
                                                                                                                       {\tt TIRNVSRCWAYETGVVLNKHEMPDQISLNDYYDYYAPDFQLHLQPSNIPNYNSPEHLSR}
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Pred. No. 9.8e
76; Mismatches
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Search completed: April 26, 2002, 17:57:28 Job time: 356 sec

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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Comp
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES OF THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).

HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence
20-AUG-2001 (Rel. 40, Last annotati
PROBABLE HISTONE DEACETYLASE (RPD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAIZE
                               PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                 InterPro; IPR000286; His_deacetylse
Pfam; PF00850; Hist_deacetyl; 1.
                                                                                                                                                             use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See I
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                Hydrolase;
                                                                                                        EMBL; AF035815; AAC50038.1;
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YUDIDIHHGDGVEEAFYATDRVMTVSFHKFGDYFPGTGHIQDIGYGSGKYYSLNVPLDDG
                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation een the Busis Institute of Bioinformatics and the EMBL outstation een the Swiss Institute. There are no restrictions on its
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                                                                                                                                          s requires a license agreement (S an email to license@isb-sib.ch).
Nuclear protein.
513 AA; 57546 MW;
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P56517;
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         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
20-AUG-2001 (Rel. 40, Last anno
HISTONE DEACETYLASE 1 (HDI).
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                  Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                          Archosauria;
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                                                                        SUBUNIT: FORMS A COMPLEX WITH RBAP48 (BY SIMILARITY) SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL). SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACU
                                                                                                               REGULATION, CELL SIMILARITY).
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Pred. No. 7.7e-118;
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                                                                                                                                                                                                MOUSE
                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
TISSUE=Fibroblast;
MEDLINE=97415582; PubMed=9271381;
                                                                                        Mus musculus (Mouse)
                                                                                                       HDAC1.
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PRINTS; PR01271; HJSDACETLASE.
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mes 270; Conserv
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Pred. No. 2.8e
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                                                                                                                              update)
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                                                                          Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .8e-114;
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                                                               Muridae;
                                                                                                                                                                                                                                                   461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKWFKRVLYIDIDVHHGDGV

195 123

255 183

243

KYHSDDYIKFLRSIRPDNMSEYS--KQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVK RFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVK 135 GTKRKYCYYYDGDYGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKANAEEMT 65

EEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRP LNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGV

EEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNYPLRDGIDDESYEAIFKP

184 196 124 136

256

244

В Š В

66 76 Matches

267;

Conservative

16

GRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIG

Query Match Best Local Similarity

57.6%; 58.9%; 77;

Score 1466; DB 1; Pred. No. 1.3e-113;

Length Indels

Mismatches

101;

8

Gaps

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364

QRLFENLRMLPHAPGVQMQAIPE-DAIPEESGDEDEEDPDKRISICSSDKRIACEEEFSD NTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPR----XWSGTATYESDSD TIRNVARCWTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNONTNEYLEKIK TIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIR

304

363

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EMBL; U80780; ADDITION OF THE CONTROL OF THE CONTRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RESPONSIBLE FOR THE DEACETYLARION OF LYSINE RESIDUES OF THE UNITERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bartl S., Taplick J., Lagger G., Khier H., Kuchler K., Seiser C.; "Identification of mouse histone deacetylase 1 as a growth factor inducible gene."; Mol. Cell. Biol. 17:5033-5043(1997).
Hydrolase; Nuclear protein.
SEQUENCE 482 AA; 55075 MW;
                                                                        PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE
                                                                                                                                                                                                                                                                      EMBL; X98207; CAA66870.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                        send an email to license@isb~sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR.
TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHER LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: FORMS A COMPLEX WITH RBAP48 (BY SIM COMPLEX WITH SIN3 AND SAP18 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).

FUNCTION: ACTS AS A TRANSCRIPTIONAL REPRESSOR.

SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAMILY. HD SUBFAMILY 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BELONGS TO THE HISTONE DEACETYLASE / ACUC
    7F64D3C17F5E4844 CRC64
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423 SDEEGEGGRKNSSNFKKAKRVKTEDEKEKDPEE 455

431 DDDKPLHGYSCRGGATTDRDSTGEDEMDDDNPE 463

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                                                                                                                                                                        Query Match
Best Local Similarity
Matches 270; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang W.-M., Inouye C.J., Zeng Y., Bearss D., Seto E.;
"Transcriptional repression by YYI is mediated by interaction with a
mammalian homolog of the yeast global regulator RPD3.";
Proc. Natl. Acad. Sci. U.S.A. 93:12845-12850(1996).
Proc. Natl. Acad. Sci. U.S.A. 93:12845-12850(1996).
PROC. Natl. Acad. Sci. U.S.A. 93:12845-12850(1996).
THE N.TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
HISTONE DEACETYLASE 2 (HD2) (YY1 TRANSCRIPTION FACTOR BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               entitles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Lymphoma;
MEDLINE-97075080; PubMed-8917507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                        PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1097691; Hdac2.
InterPro; IPR000286; His_deacetylse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HDAC2 OR YY1BP
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                                                                                                                                                                                                                                                                                                     Hydrolase; Nuclear
 136 LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGV
                                    67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: NUCLEAR. SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAMILY. HD SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: FORMS TRANSCRIPTIONAL REPRESSOR COMPLEXES BY AT LEAST WITH THE ZINC-FINGER TRANSCRIPTION FACTOR YYLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: FORMS A HETEROLOGOUS COMPLEX WITH YY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY SIMILARITY).
                                                                                                                         GRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIG 75
                                  KYHSDEYIKFLRSIRPDNMSEYS--KQMQRFNVGEDCPVFDGLFEFCQLSTGGSVAGAVK 124
                                                                                                        GGKKKVCYYYDGDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKATAEEMT 66
                                                       RFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVK 135
                                                                                                                                                                                                                                                                                                                                                     PF00850; Hist_deacetyl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          U31758; AAC52889.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                    488 AA;
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                                                                                                                                                                                           57.6%;
60.3%;
                                                                                                                                                                                                                                                                    55302 MW;
                                                                                                                                                                              68;
                                                                                                                                                                                           Score 1465.5; D
Pred. No. 1.4e-1
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                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                             Length 488,
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                                                                                                                                                          HDA1_HUMAN STANDARD; PRT; 482 AA. Q13547; Q92534; Q1-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) HISTONE DEACETYLASE 1 (HD1).
                                                                                                            -:- SUBCELLULAR LOCATION: NUCLEAR.

-:- TISSUE SPECIFICITY: UBIQUITOUS, WITH HIGHER LEVELS IN HEART,
-PANCREAS AND TESTIS, AND LOWER LEVELS IN KIDNEY AND BRAIN.
-:- SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
                                                                                                                                                                                                                                                                                                                  MEDLINE=96244606; PubMed=8646880;
                                                                                                                                                                                                                                                                                                                                                                              "A mammalian histone deacetylase related regulator Rpd3p.";
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96185499; PubMed=8602529; Taunton J., Hassig C.A., Schreiber S.L.;
                                                                                                                                                                                                                                                                                         Akiyama T., Nakamura Y.
                                                                                                                                                                                                                                                                                                                                  TISSUE-Fetal
                                                                                                                                                                                                                                                                                                                                                                    Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HDAC1 OR RPD3L1
                                                                                                                                                                                                                                                                                                     Furukawa Y., Kawakami T., Sudo K., Inazawa J., Matsumine A.,
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                               FAMILY. HD SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - - I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEAFYTTDRVMTVSFHKYGEYFPGTGDLRDIGAGKGKYYAVNFPMRDGIDDESYGQIFKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
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                                                                                                                                                                                                    091695;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE HISTONE DEACETYLASE 1-1 (HD1) (MATERNALLY-EXPRESSED
              "Xenopus HDm, a maternally expressed histone deacetylase,
an ancient family of acetyl-metabolizing enzymes.";
Gene 198:275-280(1997).
                                                                                                                                                 HISTONE DEACETYLASE) (HDM) (AB21).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                               XENLA
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MIM; 601241;
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                                                              TISSUE-Occyte;
MEDLINE-98036059; PubMed-9370292;
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PRINTS; PR01271; HISDACETLASE.
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                                                                                              SEQUENCE FROM N.A.
                                                                                                                                        Xenopodinae;
                                                                                                                                                                                                                                                                                 HD11_XENLA
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FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES
                                                                                                                                                                                                                                                                                                                                                     I-----SICSSDKRIACEEEFSDSEEE 426
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                                                                                                                                                                                                                                                                                                                                                                               LHGYSCRGGATTDRDSTGEDEMDDDNPE
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                                                                                                                                     Xenopus.
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55103 MW; 4D35B7C1ED7838D6 CRC64;
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Pred. No. 2.5e-113;
9; Mismatches 80;
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DOMAIN 299 302
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PRINTS; PR01271; HISDACETLASE.
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SUBGELUHAR LOCATION: NUCLEAR (BY SIMILARITY).

TISSUE SPECIFICITY: OCCYTE.

DEVELOPMENTAL STACE: ACCUMULATES IN PREVITELLOGENIC OCCYTES AND IS

MAINTAINED AT CONSTANT LEVEL THROUGHOUT OCCENESIS AND INTO EARLY

EMBRYOGENESIS. DECLINES THROUGH GASTRULA TO NEURULA. NOT

DETECTABLE BETWEEN NEURULA AND TAILBUD, NOR IN ADULT TISSUES OTHER

THAN OVARY.
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                                                      LHGYSCRGGATTDRDSTGEDEMDDDNPE 463
                                                                                                                    QRLFENLRMLPHAPGVQMQAVAE-
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Pred. No. 7.7e-113;
75; Mismatches 80;
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7B831822235DADB5 CRC64;
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RESULT 8
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HD12_XENLA O42227;

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE HISTONE DEACETYLASE 1-2 (HD1) (RPD3 HOMOLOG).
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DOMAIN 299 302
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Pfam; PF00850; Hist_deacetyl; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patterton D., Wolffe A.P.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
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PRINTS; PR01271; HISDACETLASE
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HISTORE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
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                                    QRLFENLRMLPHAPGVQMQAIPE----DSVHDD---
                                                                        NTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDDDDKP
                                                                                                           TIRNVARCWTYETAVALDSEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIK
                                                                                                                                             TIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIR
                                                                                                                                                                                   VMTKVMEMFQPSAVVLQCGADSLSGDRLGCFNLTIKGHAKCVEFIKTFNLPMLMLGGGGY
                                                                                                                                                                                                                      LIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGY
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Pred. No. 1.4e-112;
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between
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                               EMBL; AF026949; AAC23917.1; FlyBase; FBgn0015805; Rpd3
                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
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Nature 384:589-591(1996).
                                                                      CONFLICT
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                                                                                                                                                    Pfam; PF00850; Hist_deacetyl;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97113416;
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                                                                                                              Hydrolase;
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HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY SIMILARITY). IN DROSOPHILA, IT IS INVOLVED IN POSITION-EFFECT VARIEGATION (PEV) AND IS DIRECTLY INVOLVED IN COUNTERACTING GENOME SILENCING.

SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).

SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA FAMILY. HD SUBFAMILY 1.
                                                                                                                                                                                                                                                                                        ween the Swiss Institute of Bioinf
European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
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and this statement is not removed.
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    58183
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DI -> EIY (IN REF. 2).
C -> S (IN REF. 2).
D -> N (IN REF. 2).
E -> D (IN REF. 2).
V -> VV (IN REF. 2).
L -> V (IN REF. 2).
S -> T (IN REF. 2).
D02EA3DBD3C64688 CRC6.
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KRRYSYFYEPTIGDYYYGOGHPMKPHRIRMAHSLIIHYHLHRRLEISKPSLADASDIGKF 77

Query Best [Matches

Local

al Similarity 270; Conser

Conservative

77;

Pred. No. 1.507; Mismatches Score 1453.5;

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BG

Length

29;

Gaps

6.

57.1%; 57.9%;

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RESULT 10
HDA2_HUMAN
        15-JUL-1998
15-JUL-1998
20-AUG-2001
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                              Yang W.-M., Inouye C.J., Zeng Y., Bearss D., Seto E.;
"Transcriptional repression by YY1 is mediated by interaction with a mammalian homolog of the yeast global regulator RPD3.";
Proc. Natl. Acad. Sci. U.S.A. 93:12845-12850(1996).
-!- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
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Homo sapiens (Human).
Mortazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Breast
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-97075080; PubMed=8917507;
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FORMS TRANSCRIPTIONAL REPRESSOR COMPLEXES BY A WITH MAD, SIM3, YYL AND N-COR.

SUBUNIT: FORMS A HETEROLOGOUS COMPLEX AT LEAST WITH YYL
                                                                                                                                                           SIMILARITY:
                                                                                                                                                                                               TISSUE
                                                                                                                                     FAMILY. HD SUBFAMILY
                                                                                                                                                                                                               SUBCELLULAR LOCATION: NUCLEAR.
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15-JUL-1998 (Rel. 36,
20-AUG-2001 (Rel. 40,
HISTONE DEACETYLASE 1
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MIM; 605164;
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES CORE HISTONES (HEALTH HE AND HE).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                          NCBI_TaxID-7668;
                                                                                                                                       Strongylocentrotus
                                                                                                                                                     Eukaryota; Metazoa; Echino
Echinoidea; Euechinoidea;
                                                                                                                                                                  Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; E
                                                                                                                                                                                                HDAC1
                                                                                                                                                                                                                                                                    P56518;
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                                                                                   Nemer M.;
                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                       Echinacea;
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                                                                                                                                                     Echinoida; Strongylocentrotidae;
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HDA2_CHICK
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Matches 267
                                                                                                                                                                                                           HDA2_CHICK STANDARD: PRT; 488 AA. P56519; P56519; P56519; P56519; P56519; P676519; P
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NCBI_TaxID-9031;
[1]
                                                                                                                                                   Gallus gallus (Chicken).
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                                                                                           Archosauria; Aves;
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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les 267; Conserv
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SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA FAMILY. HD SUBFAMILY 1.
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                                                                                        Neognathae;
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                                                                                           Galliformes; Phasianidae;
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                                                                                        Phasianinae,
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RESULT 13
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STANDARD; 36, 36,

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Best Local Similarity 59.4%;
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DOMAIN 300 303
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PRINTS; PR01271; HISDACETLASE.
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I---SIR---ASDKRIACDEEFSDSEDE
                                                                                                                                          TIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIR
                                                                                                                                                                                                                                                                  EEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRP
                                    LHGYSCRGGATTDRDSTGEDEMDDDNPE
                                                                  QRLFENLRMLPHAPGVQMQAIPE----DAVHED---
                                                                                              NTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDDDDKP 435
                                                                                                                                                                                      IISKVMEMYQPSAVVLQCGADSLSGDRLGCFNLTVKGHAKCVEVVKTFNLPLLMLGGGGY
                                                                                                                                                                                                                  LIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGY
                                                                                                                                                                                                                                                  {\tt EEAFYTTDRVMTVSEVSMVNNFPGTGDLRDIGAGKGKYYAVNFPMRDGIDDESYGQIFKP}
                                                                                                                                                                                                                                                                                                           LNRQQTDMAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGV
                                                                                                                                                                                                                                                                                                                                     LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGV 195
                                                                                                                                                                                                                                                                                                                                                                     KYHSDEYIKFLRSIRPDNMSEYS--KOMORFNVGEDCPVFDGLFEFCOLSTGGSVAGAVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GGKKKYCYYYDGDIGNYYYGQGHPMKPHRIRMTHNLLLNYGLYRKMEIYRPHKATAEEMT 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 AA;
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Pred. No. 4.2e-110;
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-i- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION, CELL CYCLE PROGRESSION AND DEVELOPMENTAL EVENTS (BY
                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00850; Hist_deacetyl;
PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z81486; CAB03984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase;
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                                                                                      LAAATKLNKQKVDIAINWMGGLHHAKKSEASGFCYTNDIVLGILELLKYHKRVLYVDIDV
                                                                                                                    QSIFKPIMTKVMERFDPCAVVLQCGADSLNGDRLGPFNLTLKGHGECARFFRSYNVPLMM
                                                                                                                               HHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESF
                                                                                                                                                                                                                                                                                                             SGP--DGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLA
              DDDDKPLHGYSCRGGATTDRD-STGEDEMDDDNPEPD
                                                      DMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDS
                                                                                                                                                            HHGDGVEEAFYTTDRVMTVSFHKYGDFFPGTGDLKDIGAGKGKLYSVNVPLRDGITDVSY
                                                                                                                                                                                                                           IGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDV
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                                 MLAKLQTDVIANLEQLTFVPSVQMRPIP--EDALSALNDD-
                                                                           VGGGGYTPRNVARCWTYETSIAVDKEVPNELPYNDYFEYFGPNYRLHIESSNAANENSSD
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461 AA; 52137 MW;
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                                                                                                                                                                                                                                                                                                                                             53.4%;
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TO THE HISTONE DEACETYLASE
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                                                                                                                                                                                                                                                                                                                                             Score 1359.5; DB 1
Pred. No. 7.6e-105;
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              465
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$66438;

$83226;

$246259;

$771605;

$771606;
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"HDA1 and RPD3 are members of distinct yeast histone deacetylase complexes that regulate silencing and transcription.";
Proc. Natl. Acad. Sci. U.S.A. 93:14503-14508(1996).
-I- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL REGULATION AND CELL CYCLE PROGRESSION. TO MANY GENES INCLUDING TRANSCRIPTION ARD REPRESSION AND ACTIVATION OF MANY GENES INCLUDING CELL TYPE-SPECIFIC GENES (STE6, TY2 AND HO), CELL DIFFERENTIATION-SPECIFIC GENES (SPO13), GENES THAT RESPOND TO EXTERNAL SIGNALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-S288C / FY1679;
van Dyck L., Pascual-Ahuir A.,
Submitted (DEC-1994) to the EM
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20-AUG-2001 (Rel. 40, Last annotation update)
HISTONE DEACETYLASE RPD3 (TRANSCRIPTIONAL REGULATORY PROTEIN RPD3).
RPD3 OR SDI2 OR YNL330C OR NO305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95373280; PubMed-7645347;
Maftahi M., Nicaud J., Levesque H., Gaillardin C.;
"Sequencing analysis of a 15.4 kb fragment of yeast chromosome XIV identifies the RPD3, PAS8 and KREI loci, five new open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-OCT-1993
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MEDLINE=97121415; PubMed=8962081;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rundlett S.E., Carmen A.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       reast 11:567-572(1995).
                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a cween the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content is ified and this statement is not removed. Usage by and for
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negative transcriptional states in Saccharomyces cerevisiae.
Cell. Biol. 11:6317-6327(1991).
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SUBUNIT: IT PRO
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AAB20328.1;
CAA58228.1;
CAA86368.1;
CAA96262.1;
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SIN3/RPD1. IN
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THE HISTONE DEACETYLASE /
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CPR6 AND
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P56520;
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SGD; S0005274; RPD3.
InterPro; IPR000286; His_deacetylse.
Pfam; PF00850; Hist_deacetyl; 1.
PRINTS; PR01270; HDASUPER.
PRINTS; PR01271; HISDACETLASE.
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15-JUL-1998 (Rel. 36, Last s
20-AUG-2001 (Rel. 40, Last a
HISTONE DEACETYLASE 3 (HD3).
                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Archosauria; Aves; N
                                                                                                                                                                             Takami Y
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
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                                                                               SIMILARITY).
SUBCELLULAR LOCATION: NUCLEAR
                                                                                                           REGULATION, CELL
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433 AA; 48904 N
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Pred. No. 2.5e
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Matches 237
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Pfam; PF00850; Hist_deacetyl; 1.
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                                SDSDDD
                                                                TIFENLKMLNHAPSVQIHDVPSDLLSYDRT-DEPDPEERGSEENYSRPE---
                                                                                                TLLEQLSGLIHAPSVQFQHTP----PVNRVLDEPE-----DDMETRPKPRXWSGTATYE
                                                                                                                                    RNVARCWTYETSLLVDEAISEELPYSEYFEYFAPDFTLHPDVSTRIENQNSRQYLDQIRQ
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237; Conservative
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421
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(See http://www.isb-sib.ch/announce/
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Search completed: April 26, 2002, 17:57:52 Job time: 335 sec

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Result
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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ETAVAVG	EAVVLQCO	WGGGLHH WAGGLHH TVSFHKF0 	ASVSPESI :: : RSITPET(PTIGDYY	Score 1560.5; Pred. No. 2.8e 4; Mismatches	H71071 T13964 T13964 T13964 T13964 T13964 A81926 A81926 A81926 F811747441 T74728 H75470 T727101 T727101 T727101 ALIGN AL)
NVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPME ::	:SFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSY 	ASAGGS IGAAVKLINKQDADIAINNGGGLHHAKKSEASGFCYVNDIVIGII.ELLKMFKRVL : :	SRPSLADASDIGREHSPEYVDFLASVSPESMGDPSAARNLRRENVGEDCPVFDGLFDFC :	DESGISLÞSGÞDGRKRRVGYFYÐÞFIGDYYYGOGHÞMKÞHRIRMAHSLIIHYHLHRRLEI 	1560.5; DB 2; Leng No. 2.8e-116; matches 94; Indel	MENTS 0 - Arabidopsis cress) Apr-1999 #text_o putt, R.; Bancros putt, R.; Bancros clone F20D10 BAC clone F20D10 BAC clone F20D10	
DYTLHVDPSPMI 	GHADCLRFLRS' : : : GHAECVKFMRS	ILELLKMEKRV	CPVFDGLFDFCF : : CPVFDGLYSFCQ	.IIHYHLHRRLE: : : :: LAHYGLLQHMQ)	th 501; s 31;	pothericobable robable robable retylpothericy pothericy pothericy potherics and a final and a final a	
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C; Species: Zea mays (maize)
C; Species: Zea mays (maize)
C; Species: Zea mays (maize)
C; Date: 12-Feb:1999 #sequence_revision 12-Feb-1999 #text_change 12-Nov-1999
C; Date: 12-Feb:1999 #sequence_revision 12-Feb-1999 #text_change 12-Nov-1999
C; Accession: T01413
R; Rossi, V: Hartings, H: Motto, M.
Mol. Gen. Genet. 256, 288-296, 1998
A; Title: Identification and characterisation of an RPD3 homologue from maize (Zea n A: Reference number: Z14321; MUID:98307342
A; Accession: T01413
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-513 <ROSS-
A; Cross-references: EMBL-AF035815; NID:g2665839; PIDN:AAC50038.1; PID:g2665840
A; Experimental source: strain W22
C; Genetics:
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C;Superf
C;Keywor
F;27-325
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Best Local
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                                                                                                                                                                        SYNVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSP
                                                                                                                                                                                                                                         DGMDDESFRSLFRPLIQXVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLR
                                                                                                                                                                                                                                                                                        VLYVDIDIHHGDGVEEAFYTTDRVMTVSFHKFGDYFPGTGDIRDIGHSKGKYYSLNVPLD
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                                                                                                                                                                                                                                                                                                                                                                                                                       QVYRPNPARERELCRFHAEEYINFLRSVTPETQQD--QIRLLKRFNVGEECPVLDGLYSF
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                                                                                     MENKNTRQQLDDIRS----KLSKLRHAPSVHFQERVPDTEIPEQDEDQDDPDERHDP---
                                                                                                                    MENLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRV--LDEPEDDMETRPKPRXW
                                                                                                                                                                                                                        \tt DGIDDESYQSLFKPIMGKVMEVFRPGAVVLQCGADSLSGDRLGCFNLSIKGHAECVRYMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGSGGNSLPSVGPDGQKRRVCYFYDPDVGNYYYGQGHPMKPHRIRMTHSLLARYGLLNQM
                                                     SGTATYESDSDDDD 433
                                                                                                                                                       SFNVPLLLLGGGGYTIRNVARCWCYETGVALGQEPEDKMPVNEYYEYFGPDYTLHVAPSN
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                      -DSDMEVDD 423
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Pred. No. 7.6e-113;
""matches 72;
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                                                                                                                   submitted to the EMBL Data Library, A; Reference number: z19232 A; Accession: T20163
                                                                                                                                                                                                   hypothetical protein C53A5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
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A:Gene: CESP:C53A5.3
                    C; Genetics:
                                A; Experimental source:
                                                     A;Cross-references:
                                                                 A; Molecule type: DNA
A; Residues: 1-461 <WIL>
                                                                                                 A; Status: preliminary; translated
                                                                                                                                                                      R; Mortimore,
                                                                                                                                                                                                                                                     T20163
                                                                                                                                                                                      Accession:
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T20163

EMBL: 281486; PIDN: CAB03984.1; GSPDB: GN00023; CESP: C53A5.3

from

GB/EMBL/DDBJ

November

clone

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RESULT 3
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$60381
September 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: S60381; S43160
R;Ladomery, M.R.; Lyons, S.; Sommerville, J.
submitted to the EMBL Data Library, December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X78454; NID:g773397; PIDN:CAA55211.1; C;Superfamily: RPD3 protein; RPD3/acuC homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-480 <LAD>
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A; Accession: S60381
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Best Local Similarity 59.4%; Pred. No. 4.9e-108;
405 I---SIR---SSDKRIACDEEFSDSEDE 426
                                                                                                                                                                                                                                                                                                                                  244 VMSKVMEMFQPSAVVLQCGADSLSGDRLGCFNLTIKGHAKCVEFIKTFNLPLLMLGGGGY
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                                                    LHGYSCRGGATTDRDSTGEDEMDDDNPE 463
                                                                                                                                                                                                                      TIRNVARCWTYETAVALDSEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIK
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                                                                                                              QRLFENLRMLPHAPGVQMQAVAE-----DSIHDD------SG----EEDEDDPDKR
                                                                                                                                           NTILLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDUDDKP
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R;Nicaud, J.J.
R;Nicaud, J.J.
submitted to the EMBL Data Library,
A·Description: Sequence analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 23-Mar-2001
C;Accession: S22284; S51336; S51285; S55859; S57393; S63313; S63311
C;Vidal, M.; Gaber, R.F.
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A;Title: RPD3 encodes a second factor required
A;Reference number: S22284; MUID:92049362
A;Accession: S22284
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C:Superfamily: RPD3 protein; RPD3/acuC homology
                                            A; Reference number: S51285
A; Accession: S51285
                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-433 < VAN>
                                                                                                                                                                                                                                              A; Reference number: S51334
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                                                                                                                                                   A;Cross-references: EMBL:X83226; NID:g642335; PIDN:CAA58228.1; PID:g642338
                                                                                                                                                                                                                           A; Accession: S51336
                                                                                                                                                                                                                                                                     icated gene for a putative aryl-alcohol dehydrogenase
                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, December 1994
A; Description: A 8.2 kb DNA segment from chromosome XIV
                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:S66438; NID:g238961; PIDN:AAB20328.1; PID:g238962
R;van Dyck, L.; Pascual-Ahuir, A.; Goffeau, A.
                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-433 <VID>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N; Alternate names: protein N0305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcription regulator RPD3 -
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: not compared with conceptual translation
;Molecule type: DNA :Residues: 1-201 <NIC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 QSIFKPIMTKVMERFDPCAVVLQCGADSLNGDRLGPFNLTLKGHGECARFFRSYNVPLMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 DDDDKPLHGYSCRGGATTDRD-STGEDEMDDDNPEPD 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 LAAATKLNKQKVDIAINWMGGLHHAKKSEASGFCYTNDIVLGILELLKYHKRVLYVDIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 SGP--DGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANPDKRLPPQITDGMIQDDGDFYDGEREGDDRRNESD 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MLAKLQTDVIANLEQLTFVPSVQMRPIP--EDALSALNDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SFEDMTRFHSDEYMTFLKSANPDNL--KSFNKQMLKFNVGEDCPLFDGLYEFCQLSSGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DASDIGREHSPEYVDELASVSPESMGDPSAARNLRRENVGEDCPVFDGLEDFCRASAGGS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VGGGGYTPRNVARCWTYETSIAVDKEVPNELPYNDYFEYFGPNYRLHIESSNAANENSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDV 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGPLMEHGKRRVAYYYDSNIGNYYYGQGHVMKPHRIRMTHHLVLNYGLYRNLEIFRPFPA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1359.5; DB 2;
Pred. No. 2.4e-100;
5; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein YNL330c
                                                                                      a 13.9 Kb fragment of yeast chromosome XIV identifi
                                                                                                                January 1995
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                                                                                                                                                                                                                                                                                             the RPD3 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              positive and negative
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                                                                                                                                                                                                                                                                                             PAS8
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A;Title: An 8.2 kb DNA segment from chromosome XIV carries the d gene for a putative aryl-alcohol dehydrogenase. A:Reference number: S57391; MUID:96021610 A;Accession: S57393
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A;Title: Sequencing analysis of a 15.4 kb fragment of yeast chromosome A;Reference number: S55859; MUID:95373280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: transcription regulation
C;Superfamily: RPD3 protein; RPD3/acuC homology
C;Keywords: nucleus; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: strain S288C R; Maftahi, M.; Nicaud, J.M.; Levesque, H.; Gaillardin, C. submitted to the Protein_Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:XB3226; NID:g642335; PIDN:CAA58228.1; PID:g642338
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1994
R;Coster F: Jonniaux, J.L.; Goffeau, A.; Purnelle, B.; Van Dyck, L.
submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-433 <VAW>
                                                         В
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A;Cross-references: SGD:S0005274; MIPS:YNL330c
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A; Residues: 1-433 < COS>
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Yeast 11, 9
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-201 < M
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A; Residues: 1-201 <MAW>
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258 OKVMEVYOPEAVVLOCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTI 317
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987-991,
                                                                                                          AFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLI
                                                                                                                                                               RGKCDVAVNYAGGLHHAKKSEASGFCYLNDIVLGIIELLRYHPRVLYIDIDVHHGDGVEE
                                                                                                                                                                                                                                                                                                                                                                                             KRRVAYFYDADVGNYAYGAGHPMKPHRIRMAHSLIMNYGLYKKMEIYRAKPATKQEMCQF
                                                                                                                                                                                                 RQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVEE
                                                                                                                                                                                                                                                                               HTDEYIDFLSRVTPDNL--EMFKRESVKFNVGDDCPVFDGLYEYCSISGGGSMEGAARLN
                                                      AFYTTDRVMTCSFHKYGEFFPGTGELRDIGVGAGKNYAVNVPLRDGIDDATYRSVFEPVI
                                                                                                                                                                                                                                                                                                                                   HSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVKLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1328.5; DB Pred. No. 6.4e-98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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256

KKIMEWYQPSAVVLQCGGDSLSGDRLGCFNLSMEGHANCVNYVKSFGIPMMVVGGGGYTM

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hypothetical protein R06Cl.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change C;Accession: T23963; T24071
R;Kershaw, J.
submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Molecule type: DNA
A;Residues: 1-465 <WIZ>
A;Residues: 1-465 <WIZ>
A;Cross-references: EMBL:Z81108; PIDN:CAB03240.1; GSPDB:GN000019; CESP:R06C1.1
A;Experimental source: clone R09B3
C:Genetics:
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A;Accession: T23963
A;Status: preliminary; translated from
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A:Introns: 53/3; 212/1; 279/1;
C:Superfamily: RPD3 protein; R
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A;Reference number: Z19837
A;Accession: T24071
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: Z81106; PIDN: CAB03224.1; GSPDB: GN00019; CESP: R06C1.1
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A; Residues: 1-465 <WIL>
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Best Local :
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                                                                                                                                                                     QKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IFANLENTKYAPSVQLNHTPRDAEDLGDVEED - - - SAEAKDTKGGSQYARD
                                   TLLEGLSGLIHAPSVQFQ
                                                                                                                                                   GEVMARFQPEAVVLQCGADSLAGDRLGVFNLTTYGHGKCVEYMKSFNVPLLLVGGGGYTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESD
ALLENLKOLPHVPSVQMQ
                                                                        RNVSRCWLYETAIALNQEVSDDLPLHDYFDYFIPDYKLHIKPLAALSNFNTPEFIDQTIV
                                                                                                            RNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDP-SPMENLNTPKDMERIRN
                                                                                                                                                                                                                              AFYTTDRVMTVSFHKHGEYFPGTGDLKDVGAGSGKYYALNVPLRDGVDDVTYERIFRTIM
                                                                                                                                                                                                                                                   AFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLI
                                                                                                                                                                                                                                                                                                      RQESEIAINWMGGLHHAKKSEASGFCYSNDIVLAILELLKHHKRVLYIDIDVHHGDGVEE
                                                                                                                                                                                                                                                                                                                                          RQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVEE 197
                                                                                                                                                                                                                                                                                                                                                                               HSDDYINFLRNVKSDNMS--TFTDQMARFSVGEDCPVFDGMYEFCQLSCGGSLAAAARLN
                                                                                                                                                                                                                                                                                                                                                                                                                    HSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVKLN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSRVSYYYDGDFGNFYYGQGHPMKPHRVRMTHSLIVNYGLYRKLNVMRPARASFSEITRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.3%;
61.9%;
                                     394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1305.5; DB 2;
Pred. No. 4.8e-96;
7; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB/EMBL/DDBJ
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A:Map position: 18B3
A:Introns: 19/1; 46/3; 94/2; 121/3; 140/3; 159/2; 204/1; 231/1; 252/3; 277/2; 307/2; C:Superfamily: RPD3 protein: RPD3/acuC homology C:Keywords: hydrolase; phosphoprotein E:7-307/Domain: RPD3/acuC homology <RAH1> F:232,282,404/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 263, 482-490, 1999
A; Title: Cloning and characterization of the murine histone
A; Reference number: JC7102; MUID:99423490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      histone deacetylase (EC 3.5.1.-) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-C:Accession: JC7102
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A; Residues: 1-424 < MAH>
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R;Mahlknecht, U.; Hoelzer, D.; Bucala, R.; Verdin,
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                                                                                  Вþ
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421 D 421
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nes 235; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 KTVAYFYDPDVGNFHYGAGHPMKPHRLALTHSLVLHYGLYKKMIVFKPYQASQHDMCRFH 62
                                                                                  TIFENLKMLNHAPSVQIHDVPADLLTYDRTDEADAEERGPEENYSRPEAPNEFYDGDHDN
                                                                                                                                                                                                                                                                           OKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTI
                                                                                                                      TLLEQLSGLIHAPSVQFQHTPPVNRVLDEPED-DMETRPKPRXWSGTAT----YESDSDD
                                                                                                                                                                  RNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSP-MENLNTPKDMERIRN
                                                                                                                                                                                                                                                     SQVVDFYQPTCIVLQCGADSLGCDRLGCFNLSIRGHGECVEYVKSFNIPLLVLGGGGYTV
                                                                                                                                                                                                                                                                                                                                         FYLTDRVMTVSFHKYGNYFFPGTGDMYEVGAESGRYYCLNVPLRDG1DDQSYKHLFQPV1
                                                                                                                                                                                                                                                                                                                                                                                  FYTTDRVMTVSFHKFGD-FFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVEEA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEDYIDFLORVSPINM--OGFIKSLNAFNYGDDCPVFPGLFEFCSRYTGASLQGATQLNN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVKLNR 138
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R:Dangond, F.; Hafler, D.A.; Tong, J.K.; Randall, J.; Kojima, R.; Biochem. Biophys. Res. Commun. 242, 648-652, 1998
A;Title: Differential display cloning of a novel human histone dea A; Reference number: JC5834; MUID:98125547
A; Accession: JC5834

deacetylase (HDAC3)

G

Otku, N.; Gullans,

A;Status:

nucleic

acid

sequence not

shown

histone deacetylase (EC 3.5.1.-) 3 - human C:Species: Homo sapiens (man) C:Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 12-Nov-1999

Accession: JC5834

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histone deacetylase (EC 3.5.1.*) - fission yeast (Schizosaccharomyces pombe)
%;Alternate names: cryptic loci regulator protein clr6
C;Species: Schizosaccharomyces pombe
C;Date: 03.0ec-1999  #sequence_revision 03.Dec-1999  #text_change 21-Jul-2000
C;Accession: T40300; T43796
R;Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Hilbert, H.; Moestl, D.; submitted to the EMBL Data Library, May 1998
A;Reference number: Z21919
A;Accession: T40300
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A; Residues: 1-428 <DAN>
A; Residues: 1-428 <DAN>
A; Cross-references: GB:U66914; NID:g2934900; PIDN:AAC52038.1; PID:g2326173
A; Cromment: This enzyme plays a role in multiple and complex cellular pathways of gets for the treatment of cancer and autoimmunity.
C; Superfamily: RPD3 protein; RPD3/acuC homology
                                                                                                  A:Cross-references: EMBL:AL023589; PIDN:CAA19053.1; GSPDB:GN00067; SPDB:SPBC36.
A:Experimental source: strain 972h-; cosmid c36
R:Grewal, S.I.; Bonaduce, M.J.; Klar, A.J.
Genetics 150, 563-576, 1998
A:Tittle: Histone deacetylase homologs regulate epigenetic inheritance of transc A:Reference number: 22685; MUID:98429513
A:Accession: T43796
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                           A; Molecule type: DNA
A; Residues: 1-405 <GRE>
A;Cross-references: EMBL:AF064206; NID:g4159996; PIDN:AAD05211.1; PID:g4159997
                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVVDFYOPTCIVLQCGADSLGCDRLGCFNLSIRGHGECVEYVKSFNIPLLVLGGGGYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FYTTDRVMTVSFHKFGD-FFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSP-MENLNTPKDMERIRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FYLTDRVMTVSFHKYGNYFFPGTGDMYEVGAESGRYYCLNVPLRDGIDDQSYKHLFQPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVEEA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEDYIDFLQRVSPTNM--QGFTKSLNAFNVGDDCPVFPGLFEFCSRYTGASLQGATQLNN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNVARCWTYETSLLVEEAISEELPYSEYFEYFAPDFTLHPDVSTRIENQNSRQYLDQILQ
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55.6%;
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81

EYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGS1GAAVKLNRQD 140 VFFWVAGDVGSVYFGPNHPMKPHRLCMTHHLILAYGLHSKMEVYRPHKAYPIEMAQFHSP

63

4

21 VSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIGRFHSP 80

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A:Experimental source: strain 972
c;Genetics:
A:Gene: clr6; SPBC36.05c
A:Map position: 2
A:Introns: 14/1; 34/3; 51/3; 91/1; 101/2; 116/1;
C:Superfamily: RPD3 protein; RPD3/acuC homology
C:Keywords: hydrolase; transcription regulation
                                                                                                  A;Introns: 47/3; 87/1; 112/1; 185/2; 206/3; 237/3; A;Note: T18B22.80 C:Superfamily: RPD3 protein; RPD3/acuC homology
                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein T18B22.80 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                A; Reference number: Z24467
A; Accession: T47443
                                                                                                                                                                                                                                                                                                                                                       R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, submitted to the Protein Sequence Database, February 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
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                                                                                                                                                               A; Map position: 3
                                                                                                                                                                                          C; Genetics:
                                                                                                                                                                                                           A; Experimental source: cultivar Columbia; BAC clone T18B22
                                                                                                                                                                                                                                 A; Cross-references: EMBL:AL138652
                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-419 < JOR>
                                                                                                                                                                                                                                                                                          A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 QKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 SHIMQWFRPEAVILQCGTDSLAGDRLGCFNLSMKGHSMCVDFVKSFNLPMICVGGGGYTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 FFYTTDRVMTCSFHKFGEYFPGTGHIKDTGIGTGKNYAVNVPLRDGIDDESYESVFKPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 RQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVEE
                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         I I ENLRNLSFAPSVQMHKTP
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Conservative
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                 47.4%; Score 1207; DB 2; 53.4%; Pred. No. 2.8e-88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         382
71; Mismatches
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                                         DB 2;
  109;
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                                                                                                                                              270/1; 286/3; 317/1; 340/3; 373/3;
                                     Length 419;
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Indels
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16;
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A;Description: involved in the meiotic ce
;Superfamily: RPD3 protein; RPD3/acuC ho
C;Keywords: hydrolase
F;30-330/Domain: RPD3/acuC homology <RAC>
                                                                                                                                                                                                                                                                                                                                                      C:Genetics:
A;Gene: hdal; Phdl; SPAC3G9.07c
A;Map position: IL
C:Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Phd1+, a histone deacetylase gene of Schlzosaccharomyces pombe, is required A;Reference number: Z22404; MUID:98452937
A;Accession: T43300
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-434 <KIM>
A;Cross-references: EMBL:AB008888; NID:92641698; PIDN:BAA23598.1; PID:92641699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      histone deacetylase (EC 3.5.1.-) - fission yeast (Schizosaccharomyces N;Alternate names: Phdl protein C:Species: Schizosaccharomyces pombe C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul C:Accession: T11643; T43300
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R;Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, December 1997
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R;Kim, Y.B.; Honda, A.; Yoshida, M.; Horinouchi,
FEBS Lett. 436, 193-196, 1998
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A; Residues: 1-434 <WOO>
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A; Accession: T11643
                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                      Local Similarity
nes 207; Conserv
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    FHREDYLDFLKRVTPDNA--EQFADKFQQFNIGDDCPVFDGTYEFSQRSAGASLDASRKL
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                                                                                   QKKRVTYHLDEQVGNYHYGDKHPMKPHRITITNHLVMGYGLHNKMSVFSPRMATFGEMSE
                                                                                                                       RKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIGR 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENLRYIQHAPSVQMQEVPPDFYIPDFDEDEQNPDVRADQRSRDK-QIQRDDEYFDGDNDN 416
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                                          FHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVKL 136
                                                                                                                                                                   Conservative
                                                                                                                                                                                       44.9%;
53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 1143.5; DB 2; Length
; Pred. No. 3.3e-83;
73; Mismatches 100; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein C08B11.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 31-Jan-2000 C;Accession: T19067
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A; Introns: 45/1;
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A; Residues: 1-507 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Sims, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: clone C08B1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z46676; PIDN:CAA86662.1; GSPDB:GN00020; CESP:C08B11.2
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Best Local Similarity
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                                                                                                                                                                                                                               184 YIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDG
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                                                                                                                                                                                                                                                                                                                                 124 ASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 LRIRALEQLRYLGGAPSVQMQQIPP
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                                                                                                                                                                                                                                                                                                                                                                          VESPKLDAADISVFHTEDYVNFLQTVTPK-LGLTMPDDVLRQFN1GEDCP1FAGLWDYCT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNDEITEPDGADVKKRNVAYYYHKDVGHFHYGQLHPMKPQRLVVCNDLVVSYEMPKYMTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGY
                                          GKPLMVLGGGGYTLRNVARCWALETGVILGLRMDDEIPGTSLYSHYFTPRLLRPNLVPKM
                                                                              NVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNE-YFEYFGPDYTLHVDPSPM
                                                                                                                     | INDEPYLIKLTESYISGVEENFNPEAIVLQCGSDSLCEDRLGQFALSFNAHARAVKYYKSL
                                                                                                                                                                                                            YIDIDIHHGDGVQEAFNNSDRVMTVSFHRFGQYFPGSGSIMDKGVGPGKYFAINVPLMAA
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ENLINTPROMERIRATILEQUISGUIHAPSVQFQHTPPVNRVLDEPEDDMETRERPRIMSGT
                                                                                                                                                                 MDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSY
                                                                                                                                                                                                                                                                                                                                                                                                                  SRPSLADASDIGRFHSPEYYDFLASYSPESMGDPSAARNLRRFNYGEDCPYFDGLFDFCR 123
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44.6%;
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Pred. No. 5.3e-75;
0; Mismatches 171;
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A:Map position: 7L
C:Superfamily: RPD3 protein; RPD3/acuC homology
F:30-331/Domain: RPD3/acuC homology <RAH1>
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N;Alternate names: hypothetical protein G1330
C:Species: Saccharomyces cerevisiae
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 20-Jun-2000
C:Accession: S64211; S62051
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A; Gene: SGD: HOS2
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A;Residues: 1-351,'HSGTHS',358,'RIIHET',365-452 <COG>
A;Cross-references: EMBL:X91837; NID:g1177627; PIDN:CAA62950.1;
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R;Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, submitted to the Protein Sequence Database, May 1996
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A; Accession: S62051
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R;Coglievina, M.; Delneri, D.: Zaccaria, P.; Klima, R.; Bertani, I.; Bruschi, submitted to the EMBL Data Library, September 1995
A;Description: A 6.7 Kb fragment from chromosome VII of Saccharomyces cerevis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-452 <BRU>
A; Cross-references: EMBL: Z72716; NID: g1322818; PIDN: CAA96906.1;
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A; Accession: S64211
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Best Local S
Matches 198
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      RIRNTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDDD 432
                                                                                                                                                              KVMEVYQPEAVYLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTIR
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                                                                                         NVARCWCYETAVAVGVEPDNKLPYNEYF-EYFGPDYTLHVDPSPM----ENLNTPKDME
                                                                                                                                     PLIMTFKPTLIVQQCGADSLGHDRLGCFNLNIKAHGECVKFVKSFGLPMLVVGGGGYTPR
                                                                                                                                                                                                                        YTTDRVFTLSFHKYNGEFFPGTGDLTEIGCDKGKHFALNVPLEDGIDDDSYINLFKSIVD
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                                                                                                                                                                                                                                                                                                                                   DADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVEEAF
                                                                                                                                                                                                                                                                                                                                                                                               EDYVNFLSKVSPEN-ANKLPRGTLENFNIGDDCPIFQNLYDYTTLYTGASLDATRKLINN 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVSYHFNSKVSHYHYGVKHPMKPFRLMLTDHLVSSYGLHKIMDLYETRSATRDELLQFHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIGRFHS 79
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                                                 NVSRLWTYETGILNDVLLPEDIPEDIPFRDSFGPDYSLY----PMLDDLYENKNSKKLLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.4%; Score 1003.5; DB 2; 44.0%; Pred. No. 4.8e-72; tive 86; Mismatches 127;
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                                          hypothetical protein YPR068c - yeast (Saccharomyces W;Alternate names: hypothetical protein YP9499.23c C:Species: Saccharomyces cerevisiae C:Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #. C:Accession: S50089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: acuCl
A;Gene: acuCl
C;Superfamily: acetylpolyamine aminohydrolase;
F:6-306/Domain: RPD3/acuC homology <RAH1>
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D70388
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A;Accession: D70388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Aquifex aeolicus
C;Date: 08-May_1998 #sequence_revision 08-May-1998 #text_change 31-Mar-2000
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    R;Badcock, K.; submitted to ti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: strain VF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:AE000719; NID:g2983517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-375 <AQF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 392, 353-358, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
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nes 127; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMV------LGGEGYTIRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSFHKFGDF-FP-GTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLIQKVMEVYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGLHHAKKSEASGFCYVNDIVLGILELLKM-FKRVLYIDIDVHHGDGVEEAFYTTDRVMT
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                                                                                                                                                                                                                                            RGGEVRKEVKDTL
                                                                                                                                                                                                                                                                                                                            LARAWTLIWCELSGREVPEKLNNKAKELLKSIDFEEFDDE----VDRSYM--LETLKDPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSLHQSPEYAFPFEKGFLEEIGEGKGKGYNLNIPLPKGLNDNEFLFALEKSLEIVKEVFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGMHHAFKSRANGFCYINDPAVGIEYLRKKGFKRILYIDLDAHHCDGVQEAFYDTDQVFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPESMGDPSAARNLRRFNV-GEDCPVFDGLFDFCRASAGGSIGAAVKLNRQDADIAINWG
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.; Churcher, C.M. the EMBL Data Library,
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                                                                #text_change
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                                                                  06-Feb-1998
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A;Reference number: S54059
A;Accession: S54089
A;Accession: S54089
A;Molecule type: DNA
A;Residues: 1-470 <BAD>
A;Residues: 1-470 <BAD>
A;Cross-references: EMBL:249219; NID:9805025; PID:9805048; MIPS:YPR068c
A;Experimental source: strain AB972
C;Genetics:
A;Gene: SGD:HOS1
A;Gene: SGD:HOS1
A;Gross-references: SGD:S0006272; MIPS:YPR068c
A;Map position: 16R
C;Superfamily: RPD3/acuC homology
F;9-383/Domain: RPD3/acuC homology <RAH1>
Search completed: April 26, 2002, 17:52:47 Job time: 110 sec
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Matches 104; Conservat
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                                                                                                                                                                                          317 LIERHEPEALIIECGGDGLLGDRENEWQLTIRGLSRIINIMKSYPRAHIFLLGGGGYND 376
                                                                                                                                                                                                                                                                              260 YSKQIQTISVHLYEPGFFPGTGSLSDSRKDKN---VVNIPLKHGCDDNYLELIASKIVNP 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 INNSEVPTNDKPTDTYILNSETKQYNLEGDCPIFSYLPMYCQVITGATLNLLDHLSPTER 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
                                                                                                          377 LLMSRFYTYLT 387
                                                                                                                                                                                                                             260 VMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHAD-CLRFLRSY-NVPLMVLGGEGYTI 317
                                                                                                                                                                                                                                                                                                  201 TTDRVMTVSFHKF-GDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLIQK 259
                                                                                                                                                                                                                                                                                                                                                                200 LIGINWDGGRHHAFKQRASGFCYINDVYLLIQRLRKAKLNKITYVDFDLHHGDGVEKAFQ 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.1%; Score 436; DB 2; Length 470; ilarity 28.0%; Pred. No. 6.8e-27; Conservative 67; Mismatches 116; Indels
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Maximum DB seq length: 2000000000
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Perfect score:
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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          Maximum Match
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Gapop 10.0 , Gapext 0.5
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2544
1 MEADESGISLPSGPDGRKRR.....TGEDEMDDDNPEPDYNPPSS
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Copyright (c) 1993 - 2000 Com
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| RESULT 1 US-09-282-305-2 IS-equence 2, Application US/09282305 Sequence 2, Application US/09282305 Sequence 2, Application US/09282305 Patcent No. 6287943 GENERAL IMPOWANION: APPLICANT: Baidwin, Donald A. APPLICANT: Baidwin, Donald A. APPLICANT: Baidwin, Donald A. APPLICANT: Crane, Virginia C. ITITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44 FILE REFERENCE: 5718-44 FILE REFERENCE: 5718-44 FILE OF INVENTION: MUMBER: 60,080,563 PRIOR FILING DATE: 1999-03-31 PRIOR PLICATION NUMBER: 60,080,563 PRIOR PLICATION NUMBER: | 176 I WINDURANTANDE DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DEL COMPANIO DE LA COMPANIO DEL COMPANIO DELICA DEL COMPANIO DE LA COMPANIO DEL COMPANIO DEL COMPANIO DELICA DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DELICA DEL COMPANIO DEL COMPANIO DEL COMPANIO DEL COMPANIO DELICA DEL COMPANIO DEL COMPANIO DELICA DEL COMPANIO DELICA DE | . 176 LKMFKRVLYIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYA 23 | . 176 IWWEXRULYIDIDUHHAANAFAFAFATANBUWTURSHKEADEFAATANIATUTTUTTATANA 23 | | 117 DGLFPFCQASAGGSIGAAVKLNRGDADITVNWAGGLHHAKKSEASGFCYVNDIVLAILEL 17 | | 116 DGLFDFCRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILEL 17 | 116 DGLFDFCRASAGGSIGAAVKLNRODADIAINWGGGLHHAKKSEASGFCYVNDIVLGILEL 17
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 | ches 328; Conservative 50; Mismatches 73; Indels 22; Gap | t Local Similarity 69.3%; Pred. No. 1.5e-183; | ry Match 68.2%; Score 1734; DB 4; Length 45 | ; SEQ ID NO 2 | ; SOFTWARE: PatentIn Ver. 2.0 | NUMBER OF SEQ ID NOS: 18
 | PRIOR FILING DATE: 1998-04-03 | PRIOR APPLICATION NUMBER: 60/080,56 | CURRENT APPLICATION NUMBER: US/09/282,30 | GIRDENE ADDITIONATION NUMBER - TG (00 000 00 | TITLE OF INVENTION: Maize Histone Deacetylases And Their Us | APPLICANT: Crane, Virginia C.
 | APPLICANI BOILD A | ; GENERAL INFORMATION: | Patent No. 6287843 | Sequence 2, Application US/0928230 | -09-282-305-2 | RESULT 1 |
 | ALIGNMENTS | | 5 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl | 4 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl | 2 83 3.3 550 2 US-08-905-817-5 Sequence 5, Appl
 | 1 83 3.3 550 1 US-08-348-891A-5 Sequence 5, Appl | 0 83 3.3 417 5 PCT-US92-06965A-25 Sequence 25, App | 9 83 3.3 417 4 US-08-867-611-20 Sequence 20, App | 8 83.5 3.3 435 1 US-08-484-106-12 Sequence 12, App | 7 R3 S 3 3 A3S 1 NC:-08982-08983A-13 Sequence 13, App
 | 5 84 3.3 541 4 US-08-867-611-8 Sequence 8, Appl | 4 84.5 3.3 767 1 US-08-446-777-8 Sequence 8, Appl | 3 85 3.3 550 4 US-09-230-944-20 Sequence 20, App | 2 85 3.3 550 1 US-08-279-700-22 Sequence 22, App | 8 85 3.3 438 3 US-08-471-913A-105 Sequence 105, Ap
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US-09-282-305-2 | NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2 | PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2 | PRIOR APPLICATION NUMBER: 60/080,56 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2 | CURRENT AFFLICATION NUMBER: 05/09/262,30 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2
 | FILE REFERENCE: 5/18-44, CURRENT APPLICATION NUMBER: US/09/282,30 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 198-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2 | TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 RIUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2 | APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1988-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2 | APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT FILING DATE: 199-03-31 PRIOR APPLICATION NUMBER: 05/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2 | APPLICANT: Baldwin, Donald A. APPLICANT: Brigs, Steven P. APPLICANT: Brigs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2 | PARTENT NO. 628/843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT APPLICATION NUMBER: 00/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2 | Sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44 CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1998-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2
 | -09-282-305-2 Sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT APPLICATION NUMBER: 05/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION STEPPE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2 | SULT 1 -09-282-305-2 -09-282-305-2 Sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44 CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1998-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 RUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2 | SULT 1 -09-282-305-2 -09-282-305-2 sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2 | ALIGNMENTS SULT 1 -09-282-305-2 Sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44 CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT APPLICATION NUMBER: 05/09/282,305 CURRENT FILING DATE: 1998-04-03 RUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -09-282-305-2 | ALIGNMENTS SULT 1 -09-282-305-2 sequence 2, Application US/09282305 Patent No. 6.87843 GENERAL INFORMATION: APPLICANT: Bridgs, Steven P. APPLICANT: Bridgs, Virginia C. TITLE OF INVENTION: Malze Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1998-04-03 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 PRIOR | ALIGNMENTS SULT 1 -09-282-305-2 -09-282-305-2 -09-282-305-2 -09-282-305-2 -09-282-305-2 -09-282-305-2 -09-282-305-2 -09-282-305-2 -09-282-305-2 -09-282-305-2 -09-282-305-2 -09-282-305-2 -09-282-305-2 ALIGNMENTS ALIGNMENT ALIGNMENTON ALIGNMENT ALIGNMENTON ALIGNMENT FILLNG DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 05/09/282,305 PRIOR FILLNG DATE: 1999-03-31 PRIOR FILLNG DATE: 1999-04-03 PRIOR FILLNG DATE: 1999-04-03 PRIOR FILING DATE: 1998-04-03 PRIOR P | A4 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 1 Sequence 2, Appl 2 Sequence 3, Appl 2 Sequence 3, Appl 2 Sequence 3, Appl 2 Sequence 4, Appl 2 Sequence 2, Appl 2 Sequence 2, Appl 2 Sequence 3, Appl 2 Sequence 3, Appl 2 Sequence 2, Appl 2 Sequence 4, Appl 2 Sequence 2, Appl 2 Sequen | 43 83 3.3 930 2 US-09-907-817-5 Sequence 2, Appl 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 938 7 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 87 2 US-07-642-734C-4 Sequence 4, Appl 46 87 3 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 47 88 3.3 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 48 83 3.3 933 4 US-09-42C-4 Sequence 2, Appl 49 89 89 89 89 89 89 89 89 89 89 89 89 89
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Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 73; Indels 22; Gap Matches 328; | Query Match 68.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap 1 MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHL 5 | Query Match 68.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap 1 MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGOGHPMKPHRIRMAHSLIIHYHL 5 | 68.2%; Score 1734; DB 4; Length 458;
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 | ry Match 68.2%; Score 1734; DB 4; Length 45 | | ; LENGTH: 458
; TYPE: PRT
; ORGANISM: Zea mays | ; SEQ ID NO 2
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Zea mays | ; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENCTH: 458
; TYPE: PRT
; ORGANISM: Zea mays
 | NUMBER OF SEQ ID NOS: 18 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays | PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 SEQ ID NO 2 TYPE: PRT ORGANISM: Zea mays | PRIOR APPLICATION NUMBER: 60/080,56 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays | CURRENT AFFLICATION NUMBER: 05/09/262,30 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 198-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays | FILE REFERENCE: 5/18-44, CURRENT APPLICATION NUMBER: US/09/282,30 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 RUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays ORGANISM: Zea mays | TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -00-287-105-2 | APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone
Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/80,563 PRIOR PILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -00-282-105-2 | APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/80,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays | APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 SEQ ID SEC | GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Eriggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 198-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -00-282-105-28 | Sequence 2, Application US/09282305 Patent No. 6287843 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT SPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 198-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays | -09-282-305-2 Sequence 2, Application US/09282305 Patent No. 6287843 Patent No. 6287843 APPLICANT: Brigs, Steven P. APPLICANT: Brigs, Steven P. APPLICANT: Brigs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/860,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEO ID NOS: 18 SOPTWARE: Patentin Ver. 2.0 SEO ID NO 2 LENGTH: 458 TYPE: PAT ORGANISM: Zea mays | SULT 1 -09-282-305-2 -09-282-305-2 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 198-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays -00-282-305-22 a mays | SULT 1 109-282-305-2 sequence 2, Application US/09282305 sequence 2, Application US/09282305 settent No. 6287843 GREERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT FILING DATE: 199-03-31 CURRENT FILING DATE: 199-03-31 PRIOR APPLICATION NUMBER:
60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEO ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEO ID NO 2 LENGTH: 458 TYPE: PAT ORGANISM: Zea mays -09-282-165-2 | ALIGNMENTS SULT 1 -09-282-305-2 Sequence 2, Application US/09282305 SETTICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. IIILE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT FILING DATE: 1999-03-31 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 1980-03-31 PRIOR PILING DATE: 1980-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT ORGANISM: Zea mays | ALIGNMENTS SULT 1 -09-282-305-2 -09-282-305-2 Patent No. 6287843 Patent No. 6287843 PAPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Malze Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44. CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR FILING DATE: 1999-04-03 NUMBER OF SEQ ID NOS: 18 SOPTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 TYPE: PRT ORGANISM: 2ea mays | ALIGNMENTS SULT 1 -09-282-305-2 -09-282-305 | 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 59-282-305-2 Sequence 2, Application US/09282305 Sequence 2, Application US/09282305 Patent No. 6287843 Sequence 2, Application US/09282305 Patent No. 6287843 Sequence 2, Application US/09282305 Patent No. 6287843 Sequence 3, Application US/09282305 Patent No. 6287845 Steven P. Application US/09182 Sequence P. Application US/091816 C. TITLE OF INTENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44 Sequence Sequenc | 43 83 3.3 930 2 US-09-917-5 Sequence 5, Appl 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 ALIGNMENTS AL | 41
 | 40 83 3.3 417 5 PCT-US92-0696A-25 Sequence 25, Appl 42 83 3.3 550 1 US-08-348-891A-5 Sequence 5, Appl 42 83 3.3 550 2 US-08-905-817-5 Sequence 5, Appl 43 83 3.3 933 US-08-293-728-2 Sequence 2, Appl 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 46 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 50 PATENT NO. 6207843 50 PATENT NO. 620784 50 PATENT PATENT NO. NUMBER: US/09/282305 50 PATENT FILING DATE: 1999-03-31 50 PATOR APPLICATION NUMBER: US/09/282,305 50 PATOR PATENT NO. 1999-04-03 50 PATOR PATENT NO. 1999-04-04 50 PATOR PATOR PATENT NO. 1999-04-04 50 PATOR PAT | 39 83 3.3 417 4 US-08-867-611-20 40 83 3.3 417 5 PCT-US92-06965A-25 Sequence 20, Appl 41 83 3.3 550 1 US-08-348-891A-5 Sequence 5, Appl 42 83 3.3 550 2 US-08-905-817-5 Sequence 5, Appl 43 83 3.3 933 3US-08-293-728-2 Sequence 2, Appl 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 46 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 47 92-82-305-2 Sequence 2, Appl 48 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 49 PALEANT I SEQUENCE 2, Application US/09282305 PALEANT INFORMATION: Maize Histone Deacetylases And Their Uses 40 PAPLICANT: Baldwin, Donald A. AppliCANT: Briggs, Steven P. AppliCANT: Briggs, Steven P. AppliCANT: Briggs, Steven P. AppliCANT: Watize Histone Deacetylases And Their Uses 41 PAPLICANT INFORMATION: Maize Histone Deacetylases And Their Uses 42 PILE REFERENCE: 5718-44 Sequence 2, Appl 43 PAICATION NUMBER: US/09/282,305 44 US-08-282-305 45 PAICATION NUMBER: US/09/282,305 46 PAICATION NUMBER: US/09/282,305 46 PAICATION NUMBER: US/09/282,305 47 PAICATION NUMBER: US/09/282,305 47 PAICATION NUMBER: US/09/282,305 48 PAICATION NUMBER: US/09/282,305 49 PAICATION NUMBER: US/09/282,305 40 PAICATION NUMBER: US/09/282,305 40 PAICATION NUMBER: US/09/282,305 40 PAICATION NUMBER: US/09/282,305 41 PAICATION NUMBER: US/09/282,305 41 PAICATION NUMBER: US/09/282,305 42 PAICATION NUMBER: US/09/282,305 42 PAICATION NUMBER: US/09/282,305 44 US-09-4128-884 44 PAICATION NUMBER: US/09/282305 44 US-09-41218-884 44 PAICA | 38 83.5 3.3 435 1 US-08-484-106-12 Sequence 12, Appl 39 83 3.3 417 4 US-08-867-611-20 Sequence 20, Appl 41 83 3.3 550 1 US-08-348-891A-5 Sequence 25, Appl 41 83 3.3 550 1 US-08-348-891A-5 Sequence 5, Appl 42 83 3.3 550 2 US-08-905-817-5 Sequence 5, Appl 42 83 3.3 933 4 US-08-293-728-2 Sequence 5, Appl 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 59-09-282-305-2 Sequence 2, Appl 642-734C-4 Sequence 4, Appl 643-69-69-82-108-89-1 | 30 | 35 84 3.3 541 4 US-08-867-611-8 Sequence 8, Appl 37 83.5 3.3 541 5 PCT-US92-06956A-13 Sequence 12, Appl 40 83.5 3.3 435 1 US-08-484-105-12 Sequence 12, Appl 40 83 3.3 417 5 PCT-US92-06965A-25 Sequence 20, Appl 41 83 3.3 550 1 US-08-867-611-20 Sequence 20, Appl 41 83 3.3 550 2 US-08-905-817-5 Sequence 2, Appl 42 83 3.3 550 2 US-08-905-817-5 Sequence 2, Appl 43 83 3.3 550 2 US-08-905-817-5 Sequence 2, Appl 44 83 3.3 550 2 US-08-905-817-5 Sequence 2, Appl 44 83 3.3 550 2 US-08-905-817-5 Sequence 2, Appl 45 83 3.3 3557 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 64 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 64 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 64 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 84 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 66 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 67 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 67 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 67 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 67 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 68 83 3.3 3567 2 US-07-642-734C-4 Sequence 5, Appl 68 83 3.3 3567 2 US-07-642-734C-4 Sequence 6, Appl 68 83 3.3 3567 2 US-07-642-734C-4 Sequence 6, Appl 69 83 3.3 3567 2 US-07-642-734C-4 Sequence 6, Appl 69 83 3.3 3567 2 US-07-642-734C-4 Sequence 6, Appl 69 83 3.3 3567 2 US-07-642-734C-4 Sequence 6, Appl 69 83 3.3 3567 2 US-07-642-734C-4 Sequence 6, Appl 69 83 3.3 3567 2 US-07-642-734C-4 Sequence 6, Appl 69 83 3.3 3567 2 US-07-642-734C-4 Sequence 6, Appl 69 83 3.3 3567 2 US-07-642-734C-4 Sequence 6, Appl 69 83 3.3 3567 2 US-07-642-734C-4 Sequence 6, Appl 69 83 3.3 3567 2 US-07-642-734C-4 Sequence 6, Appl 69 83 3.3 3567 2 US-07-642-734C-4 Sequence 6, Appl 69 83 3.3 3567 2 US-07-642-734C-4 Sequence 6, Appl 69 83 3 US-08-293-728-2 US-07-642-734C-4 Sequence 6, Appl 69 83 3 US-08-293-728-2 US-07-642-734C-4 Sequence 6, Appl 69 83 3 US-08-293-728-2 US | 34 84.5 3.3 767 1 US-08-446-777-8 84 3.3 541 4 US-08-67-611-8 84 3.3 541 4 US-08-67-611-8 85 84 3.3 541 5 PCT-US92-06955A-13 Sequence 13, Appl 37 83.5 3.3 435 1 US-08-484-105-12 Sequence 12, Appl 40 83 3.3 417 4 US-08-867-611-20 Sequence 20, Appl 40 83 3.3 550 1 US-08-9695A-25 Sequence 25, Appl 41 83 3.3 550 2 US-08-95-817-5 Sequence 25, Appl 42 83 3.3 93 4 US-08-98-17-2 Sequence 27, Appl 42 83 3.3 93 4 US-08-98-17-2 Sequence 27, Appl 42 83 3.3 93 4 US-08-293-728-2 Sequence 27, Appl 45 83 3.3 93 4 US-08-293-728-2 Sequence 27, Appl 45 83 3.3 3567 2 US-08-97-642-734C-4 Sequence 27, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 27, Appl 45 83 3.3 3567 2 US-08-193-74C-4 Sequence 28, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29, Appl 45 83 3.3 3567 2 US-08-293-728-2 Sequence 29,
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 | APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR FILING DATE: 1999-03-31 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT | APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION STEP 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT | APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44 CUGRENT APPLICATION NUMBER: US/09/282,305 CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 198-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT | GENERAL INCORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Eriggs, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 198-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT | Sequence 2, Application US/09282305 Patent No. 6287843 Patent INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Eriggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT | -09-282-305-2 Sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their US FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/80,563 PRIOR PATING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT | SULT 1 -09-282-305-2 -09-282-305-2 Patent No. 6287843 REMERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR PRIOR APPLICATION SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT
 | SULT 1 -09-282-305-2 -09-282-305-2 Fatent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR PETING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT | ALIGNMENTS SULT 1 -09-282-305-2 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT FILING DATE: 1999-03-31 FRIOR APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-04-03 NUMBER OF SEQ ID NOS: 18 SOFTMARE: Patentin Ver. 2.0 ENGTH: 458 TYPE: PRT | SULT 1 -09-282-305-2 Sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION UNMBER: 60/080,563 PRIOR PETLING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT | ALIGNMENTS Sequence 2, Application US/09282305 Sequence 2, Application US/09282305 Sequence 2, Application US/09282305 Sequence 3, Application US/09282305 Sequence 4, Application US/09282305 Sequence 520843 GENERAL INFORMATION: Morald A. Applicant: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44. CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 FRIOR APPLICATION NUMBER: US/09/282,305 CURRENT SEQ ID NOS: 18 SOFTMARE: Patentin Ver. 2.0 LENGTH: 458 TYPE: PRT | 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 59-421-868-2 US-07-642-734C-4 Sequence 4, Appl 09-282-305-2 Sequence 2, Application US/09282305 Patent No. 6287843 Sequence 2, Application US/09282305 Patent No. 6287843 Sequence 3, Application US/09282305 Patent Information: Baldwin, Donald A. Applicant: Baldwin, Donald A. Applicant: Briggs, Steven P. Applicant: Briggs, S | 43 83 3.3 930 2 US-08-993-781-5 Sequence 5, Appl 44 83 3.3 933 4 US-08-293-728-2 Sequence 2, Appl 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 46 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 47 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 48 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 49 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 49 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 40 9-282-305-2 Sequence 2, Appl 40 9-282-305-2 Sequence 2, Appl 41 Sequence 2, Appl 42 Sequence 2, Appl 43 83 3.3 3567 2 US-07-642-734C-4 ALIGNMENTS | 41
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| ; TYPE: PRT | OKANISH: Zed mays OKANISH: Zed mays OKANISH: Zed mays 68.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps 1 MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGGGHPMKPHRIRMAHSLIHYHL 57 | OKANISH: Zed mays OKANISH OKANISH: Zed mays OKANISH: Zed mays OKANISH: Zed mays OKAN | OKANISM: Zed mays OKANISM: Zed mays OKANISM: Zed mays OKANISM: Zed mays 68.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps 1 MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGOGHPMKPHRIRMAHSLITHYHL 57 | OKANISH: Zed mays OKANISH: Zed mays OKANISH: Zed mays OKANISH: Zed mays 68.2%; Score 1734; DB 4; Length 458; Query Match Query Match Set Local Similarity 69.3%; pred. No. 1.5e-183; Best Local Similarity 69.3%; pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps 1 MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLITHYHL 57; | OKANISH: Zed mays OKANISH: Zed mays OKANISH: Zed mays 68.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps 1 MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGGGHPMKPHRIRMAHSLIHHYHL 57 | OKANISH: Zed mays OKANISH: Zed mays OKANISH: Zed mays OKANISH: Zed mays 68.2%; Score 1734; DB 4; Length 458; Query Match G9.3%; Pred, No. 1.5e-183; Best Local Similarity 69.3%; Pred, No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps 1 MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIHYHL 57
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-09-282-305-2
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; SEQ ID NO 2
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 | NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 | PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 | PRIOR APPLICATION NUMBER: 60/080,56 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 | CURRENT AFFLICATION NUMBER: 05/09/262,30 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 | FILE REFERENCE: 5/18-44, CURRENT APPLICATION NUMBER: US/09/282,30 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 | TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44 CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 Patentin Ver. 2.0 LENGTH: 458
 | APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44 CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 | APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION 1998-04-03 RIOR APPLICATION 1998-04-03 RIOR APPLICATION 1998-04-03 RIOR FILING DATE: 1998-04-03 ROFTWARE: Patentin Ver. 2.0 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 | GEMERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION STEP 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 | PARENT NO. 628/843 ERMERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. IIILE OF INVENTION: Maile Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 FRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEO ID NO 2 LENGTH: 458 | Sequence 2, Application US/09282305 Patent No. 6287843 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 | -69-282-305-2 Sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION WIMBER: 60/080,563 PRIOR APPLICATION WIMBER: 05/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 | SULT 1 -09-282-305-2 Sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 | SULT 1 -09-282-305-2 -09-282-305-2 sequence 2, Application
US/09282305 patent No. 6287843 general Information: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/80,563 PRIOR APPLICATION NUMBER: 60/80,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 | ALIGNMENTS SULT 1 -09-282-305-2 Sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR PILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 LENGTH: 458 | SULT 1 -09-282-305-2 -09-282-305-2 Sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 CURRENT FILING DATE: 1999-03-31 PRIOR FILING DATE: 1999-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 | ALIGNMENTS SULT 1 -09-282-305-2 Sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT APPLICATION NUMBER: 1999-03-31 PRIOR APPLICATION NUMBER: 1999-03-31 PRIOR PILING DATE: 1999-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 LENGTH: 458 | 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 5-2 Sequence 2, Appl 5-2 Sequence 3, Application US/09282305 Sequence 4, Appl 62 Sequence 2, Application US/09282305 Sequence 3, Application US/09282305 Sequence 2, Application US/09282305 Sequence 3, Application US/09282305 Sequence 4, Application US/09282305 Sequence 5, Application US/09282305 Sequence 6, Application US/09282305 Sequence 7, Application US/09282305 Sequence 7, Application US/09282305 Sequence 8, Application US/09282305 Sequence 9, Application US/09282, 305 Sequence 4, Application US/09282305 Sequence 4, Application US/09 | 42 83 3.3 930 2 US-08-993-781-75 43 83 3.3 933 3 US-08-293-728-2 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 46 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 47 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 48 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 49 93 93 93 4 US-09-642-734C-4 Sequence 2, Appl 40 93 93 93 93 93 93 93 93 93 93 93 93 93
 | 41 B3 3.3 550 1 US-08-348-89JA-5 Sequence 5, Appl 42 B3 3.3 550 2 US-08-905-817-5 Sequence 5, Appl 43 B3 3.3 933 3 US-08-293-728-2 Sequence 2, Appl 44 B3 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 B3 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 B3 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 46 B3 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 47 B3 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 48 B3 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 49 B3 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 49 B3 B3 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 40 B3 | 40 83 3.3 417 5 PCT-US92-06965A-25 Sequence 25, Appl 42 83 3.3 550 1 US-08-948-891A-5 Sequence 25, Appl 43 83 3.3 550 2 US-08-905-817-5 Sequence 5, Appl 44 83 3.3 933 US-08-293-728-2 Sequence 2, Appl 44 83 3.3 933 US-08-293-728-2 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 46 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 47 99-282-305-2 Sequence 2, Application US/09282305 Sequence 3, Application US/09282305 Sequence 4, Application US/09282305 Sequence 5718-44, CURRENT FILING DATE: Histone Deacetylases And Their Uses TILE OF INVENTION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR FILING DATE: 1999-03-31 PRIOR FILING DATE: 1999-03-31 PRIOR FILING DATE: 1999-03-31 PRIOR FILING DATE: 1999-03-31 SOFTWARE: PATENTIAL DATE: 1999-03-31 PRIOR FILING DATE: 1999-03-31 SOFTWARE: PATENTIAL DATE: PATENTIAL | 39 83 3.3 417 4 US-08-867-611-20 40 83 3.3 417 5 PCT-US2-0656A-25 Sequence 20, Appl 41 83 3.3 550 1 US-08-348-891A-5 Sequence 5, Appl 42 83 3.3 550 2 US-08-948-91F-5 Sequence 5, Appl 43 83 3.3 933 US-08-995-817-5 Sequence 5, Appl 44 83 3.3 933 US-08-293-728-2 Sequence 2, Appl 45 83 3.3 933 US-08-293-728-2 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 46 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 47 99-282-305-2 Sequence 2, Appl 48 40 30 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 49 PALICANT: Briggs, Steven P. APPLICANT: Briggs, Stev | 38 83.5 3.3 435 1 US-08-484-106-12 Sequence 12, Appl 41 83 3.3 417 4 US-08-867-611-20 Sequence 20, Appl 41 83 3.3 550 1 US-08-348-891A-5 Sequence 5, Appl 42 83 3.3 550 2 US-08-348-891A-5 Sequence 5, Appl 43 83 3.3 933 4 US-08-293-728-2 Sequence 2, Appl 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 64 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 64 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 87 84 87 84 87 85 85 85 85 85 85 85 85 85 85 85 85 85 | 30 | 35 84 3.3 541 4 US-08-867-611-8 Sequence 8, Appl 37 83.5 3.3 541 5 PCT US92-06965A-13 Sequence 12, App 38 83.5 3.3 435 1 US-08-484-105-12 Sequence 12, App 38 83.5 3.3 435 1 US-08-484-105-12 Sequence 12, App 40 83 3.3 417 4 US-08-867-661-20 Sequence 20, App 41 83 3.3 550 1 US-08-348-891A-5 Sequence 25, Appl 41 83 3.3 550 2 US-08-348-891A-5 Sequence 25, Appl 42 83 3.3 550 2 US-08-393-728-2 Sequence 27, Appl 43 83 3.3 933 3 US-08-293-728-2 Sequence 27, Appl 43 83 3.3 933 4 US-09-421-868-2 Sequence 27, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 594-282-305-2 Sequence 2, Appl 65-86-2 Sequence 2, Appl 76-86-2 Sequence 3, Appl 76-86-2 Sequence 4, Appl 76-86-2 Sequence 5, Appl 76-86-2 Sequence 4, Appl 76-86-2 Sequence 4, Appl 76-86-2 Sequence 5, Appl 76-86-2 Sequence 6, Appl 76-86-2 Sequence 6, Appl 76-86-2 Sequence 6, Appl 76-86-2 Sequence 76-86-2 Sequen | 34 84.5 3.3 767 1 US-08-446-777-8 35 84 3.3 541 4 US-08-687-611-8 36 84 3.3 541 5 PCT-US92-0695A-13 Sequence 8, Appl 37 83.5 3.3 435 1 US-08-484-105-12 Sequence 12, Appl 38 83.5 3.3 435 1 US-08-484-105-12 Sequence 12, Appl 39 83.5 3.3 417 5 PCT-US92-0696A-25 Sequence 12, Appl 40 83 3.3 550 1 US-08-867-611-20 Sequence 20, Appl 41 83 3.3 550 2 US-08-95-817-5 Sequence 20, Appl 42 83 3.3 550 2 US-08-95-817-5 Sequence 2, Appl 43 83 3.3 550 2 US-08-95-817-5 Sequence 2, Appl 44 83 3.3 933 3 US-08-93-728-2 Sequence 2, Appl 45 83 3.3 933 3 US-08-93-728-2 Sequence 2, Appl 46 83 3.3 933 3 US-09-293-728-2 Sequence 2, Appl 47 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 48 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 49 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 40 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 40 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 41 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 42 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 43 83 3.3 3567 2
US-07-642-734C-4 Sequence 4, Appl 44 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 46 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 47 84 US-08-10-10-10-10-10-10-10-10-10-10-10-10-10- | 33 85 3.3 550 4 US-09-230-944-20 34 84.5 3.3 767 1 US-08-467-777-8 35 84 3.3 541 4 US-08-467-777-8 36 84 3.3 541 4 US-08-867-611-8 37 83.5 3.3 541 5 PCT-US92-0695A-13 Sequence 8, Appl 37 83.5 3.3 435 1 US-08-484-105-12 Sequence 12, Appl 40 83 3.3 417 4 US-08-867-611-20 Sequence 12, Appl 41 83 3.3 550 1 US-08-967-611-20 Sequence 22, Appl 42 83 3.3 550 1 US-08-905-817-5 Sequence 5, Appl 42 83 3.3 550 2 US-08-905-817-5 Sequence 5, Appl 43 83 3.3 933 4 US-08-293-728-2 Sequence 2, Appl 45 83 3.3 3567 2 US-08-905-817-5 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 5, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 5, Appl 45 85 85 85 85 85 85 85 85 85 85 85 85 85 | 29 85 3.3 438 4 US-08-485-264A-105 Sequence 105. Appl 31 85 3.3 550 1 US-08-279-700-20 Sequence 20. Appl 33 85 3.3 550 1 US-08-279-700-20 Sequence 20. Appl 33 85 3.3 550 1 US-08-279-700-20 Sequence 20. Appl 34 84.5 3.3 550 1 US-08-446-777-8 Sequence 20. Appl 35 84.5 3.3 567 1 US-08-446-777-8 Sequence 20. Appl 36 84.5 3.3 541 5 PCT-US92-06955A-13 Sequence 13. Appl 37 83.5 3.3 435 1 US-08-446-105-12 Sequence 13. Appl 38 83.5 3.3 435 1 US-08-484-105-12 Sequence 20. Appl 40 83 3.3 437 4 US-08-867-611-20 Sequence 20. Appl 41 83 3.3 550 2 US-08-967-611-20 Sequence 20. Appl 42 83 3.3 550 2 US-08-348-105-12 Sequence 20. Appl 44 83 3.3 550 2 US-08-348-105-12 Sequence 20. Appl 44 83 3.3 933 3 US-08-967-611-20 Sequence 20. Appl 44 83 3.3 933 3 US-08-967-611-20 Sequence 20. Appl 44 83 3.3 933 3 US-08-967-611-20 Sequence 20. Appl 44 83 3.3 933 3 US-08-967-817-5 Sequence 20. Appl 44 83 3.3 933 3 US-08-967-817-5 Sequence 20. Appl 44 83 3.3 933 3 US-08-93-728-2 Sequence 20. Appl 44 83 3.3 933 3 US-08-93-728-2 Sequence 20. Appl 45 83 3.3 933 3 US-08-93-728-2 Sequence 20. Appl 46 83 3.3 933 3 US-08-93-728-2 Sequence 20. Appl 47 83 83 3.3 933 3 US-08-293-728-2 Sequence 20. Appl 48 83 3.3 933 3 US-08-93-728-2 Sequence 20. Appl 48 83 3.3 933 3 US-08-293-728-2 Sequence 20. Appl 49 83 3.3 933 4 US-09-421-868-2 Sequence 20. Appl 49 83 3.3 933 3 US-08-293-728-2 Sequence 20. Appl 49 83 3.3 933 4 US-09-421-868-2 Sequence 20. Appl 49 83 3.3 933 4 US-09-421-868-2 Sequence 20. Appl 49 83 3.3 933 4 US-09-421-868-2 Sequence 20. Appl 49 83 3.3 933 4 US-09-421-868-2 Sequence 20. Appl 49 83 3.3 933 4 US-09-421-868-2 Sequence 20. Appl 49 83 3.3 933 4 US-09-421-868-2 Sequence 20. Appl 49 83 3.3 933 4 US-09-421-868-2 Sequence 20. Appl 49 83 3.3 933 4 US-09-421-868-2 Sequence 20. Appl 49 83 3.3 933 4 US-09-421-868-2 Sequence 20. Appl 49 83 3.3 933 4 US-09-421-868-2 Sequence 20. Appl 49 83 3.3 933 4 US-09-421-868-2 Sequence 20. Appl 49 83 93 4 US-09-421-868-2 Sequence 20. Appl 49 83 93 4 US-09-421-868-2 Sequence 20. Appl 49 83 93 4 US-09-421-868-2 Se | 28 85 3.3 438 3 US-08-471-913A-105 30 85 3.3 438 4 US-08-471-913A-105 30 85 3.3 438 4 US-08-279-700-18 31 85 3.3 550 1 US-08-279-700-18 32 85 3.3 550 1 US-08-279-700-20 32 85 3.3 550 1 US-08-279-700-20 32 85 3.3 550 4 US-08-279-700-20 33 85 3.3 550 4 US-08-279-700-20 34 84 8.5 3.3 550 4 US-08-879-700-20 35 84 3.3 550 4 US-09-279-700-20 36 84 3.3 550 4 US-09-230-944-0 37 83.5 3.3 435 1 US-08-867-611-8 38 83.5 3.3 435 1 US-08-867-611-8 39 83.5 3.3 435 1 US-08-484-106-12 39 83 3.3 435 1 US-08-484-106-12 39 83 3.3 417 5 PCT-US92-0695A-25 39 83 3.3 347 5 PCT-US92-0695A-25 39 844 3.3 3.3 550 1 US-08-867-611-20 39 83 3.3 347 5 PCT-US92-0695A-25 39 844 3.3 3.3 550 1 US-08-867-611-20 39 83 3.3 347 5 PCT-US92-0695A-25 39 84 3.3 3.3 417 5 PCT-US92-0695A-25 39 84 4 US-09-484-106-12 39 84 3.3 3.3 417 5 PCT-US92-0695A-25 39 84 4 US-09-4642-734C-4 39 84 3 3.3 3.3 417 5 PCT-US92-0695A-25 39 84 4 US-09-4642-734C-4 39 84 3 3.3 3.3 417 5 PCT-US92-0695A-25 39 84 4 US-09-4642-734C-4 3 83 3.3 3.3 417 5 PCT-US92-0695A-25 39 84 4 US-09-4642-734C-4 3 84 3 3.3 3.3 417 5 PCT-US92-0695A-25 39 84 4 US-09-4642-734C-4 3 85 86 4 US-09-4642-734C-4 4 86 4 US-09-4642-734C-4 4 86 4 US-09-464 |
| ; LENGTH: 458 | TYPE: PRT ORGANISM: Zea mays 68.2%; Score 1734; DB 4; Length 458; Query Match Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps 1 MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGGGHPMKPHRIRMAHSLIHYHL 57 | TYPE: PRT ORGANISM: Zea mays 68.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps 1 MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGGGHPMKPHRIRMAHSLIHYHL 57 | TYPE: PRT ORGANISM: Zea mays ORG | TYPE: PRT ORGANISM: Zea mays 68.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGOGHPMKPHRIRMAHSLIHYHL 57 | TYPE: PRT ORGANISM: Zea mays 68.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps 1 MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGGGHPMKPHRIRMAHSLIHYHL 57 | TYPE: PRT ORGANISM: Zea mays ORGANISM: Zea mays OP-282-305-2 Query Match G8.28; Score 1734; DB 4; Length 458; Best Local Similarity 69.38; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYGOGHPMKPHRIRMAHSLIHYHL 57 MASGEGASLPSPAGGEDAHRRRVSYFYEPSIGDYYYGOGHPMKPHRIRMAHSLYVHYGL 60 SB HRRLEISRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSA-ARNLRRENVGEDCPVF 11
 | TYPE: PRT ORGANISM: Zea mays 68.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps 1 MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGGGHPMKPHRIRMAHSLIHHHL 57 | TYPE: PRT ORGANISM: Zea mays ORGANISM: Zea mays OP-282-305-2 Query Match G8.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps | TYPE: PRT ORGANISM: Zea mays ORGANISM: Zea ma | TYPE: PRT ORGANISM: Zea mays ORGANISM: Zea mays OP-282-305-2 Query Match 68.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Maches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 22; Gaps Matches 328; Conservative 50; Mismatches 73; Indels 73; | TYPE: PRT ORGANISM: Zea mays ORG | TYPE: PRT ORGANISM: Zea mays 68.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Indels 22; Gap Best Local Similarity 69.3%; Pred. No. 1.5e-183; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 10; Mismatches 10; Indels 12; Gap Matches 328; Conservative 10; Mismatches 10; Indels 12; Gap Matches 328; Conservative 10; Mismatches 10; Indels 12; Gap Matches 328; Conservative 10; Mismatches 10; Indels 12; Gap Matches 328; Conservative 10; Mismatches 10; Indels 12; Gap Matches 328; Conservative 10; Mismatches 10; Indels 12; Gap Matches 328; Conservative 10; Mismatches 10; Indels 12; Gap Matches 328; Conservative 10; Mismatches 10; Indels 12; Gap Matches 328; Conservative 10; Mismatches 10; Indels 12; Gap Matches 328; Conservative 10; Mismatches 10; Indels 12; Gap Matches 328; Conservative 10; Mismatches 10; Indels 12; Gap Matches 328; Conservative 10; Mismatches 10; Indels 12; Gap Matches 328; Conservative 10; Mismatches 10; M | TYPE: PRT ORGANISM: Zea mays ORGANISM: Zea mays -09-282-305-2 -09-282-305-2 Query Match G8.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHL 5 | TYPE: PRT ORGANISM: Zea mays ORGANISM: Zea mays OP-282-305-2 -09-282-305-2 GRANISM: Zea mays 68.2%; Score 1734; DB 4; Length 458; Query Match Best Local Similarity 69.3%; Pred. No. 1.5e-183; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap 1 MEADESGISLPSGPDGRKRRVSYFYEPTIGDYYYGOGHPMKPHRIRMAHSLIIHYHL 5 | TYPE: PRT ORGANISM: Zea mays ORGANISM: Zea mays -09-282-305-2 Query Match 68.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap
 | TYPE: PRT ORGANISM: Zea mays ORGANISM: Zea mays -09-282-305-2 Query Match 68.2%; Score 1734; DB 4; Length 458; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap | TYPE: PRT ORGANISM: Zea mays ORGANISM: Zea mays -09-282-305-2 -09-282-305-2 Guery Match 68.2%; Score 1734; DB 4; Length 458; Guery Match Best Local Similarity 69.3%; Pred. No. 1.5e-183; Best Local Similarity 69.3%; Pred. No. 1.5e-183; Matches 328; Conservative 50; Mismatches 73; Indels 22; Gap | TYPE; PRT ORGANISM: Zea mays -09-282-305-2 Ruery Match Best Local Similarity 69.3%; Pred. No. 1.5e-183; | TYPE: PRT ORGANISM: Zea mays -09-282-305-2 Query Match 68.2%: Score 1734: DB 4: Length 45 | ; TYPE: PRT;
; ORGANISM: Zea mays
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 | | ; SEQ ID NO 2 | ; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2 | NUMBER OF SEQ ID NOS: 18 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2 | PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2
 | PRIOR APPLICATION NUMBER: 60/080,56 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 | CURRENT AFFLICATION NUMBER: 05/09/262,30 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 | FILE REFERENCE: 5/18-44, CURRENT APPLICATION NUMBER: US/09/282,30 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 RUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 | TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 PRIOR PR | APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR PILICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 | APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 | GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT FILING DATE: 199-03-31 PRIOR APPLICATION NUMBER: 05/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 | PARTENT NO. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: MAIZE Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1999-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR FILING DATE: 1998-04-03 RUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2 | Sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44 CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT FILING DATE: 1998-03-31 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR APPLICATION NUMBER: 05/080,563 PRIOR APPLICATION NUMBER: 05/080,563 PRIOR APPLICATION NUMBER: 05/080,563 PRIOR PRI | -09-282-305-2 Sequence 2, Application US/09282305 Sequence 2, Application US/09282305 Patent No. 6287843 GENERAL INFORMATION: APPLICANT: Baldwin, Donald A. APPLICANT: Briggs, Steven P. APPLICANT: Crane, Virginia C. TITLE OF INVENTION: Maize Histone Deacetylases And Their Us FILE REFERENCE: 5718-44, CURRENT APPLICATION NUMBER: US/09/282,305 CURRENT APPLICATION NUMBER: 05/080,563 PRIOR APPLICATION NUMBER: 60/080,563 PRIOR PILING DATE: 1998-04-03 NUMBER OF SEQ ID NOS: 18 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2
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83 3.3 550 2 US-08-905-817-5 Sequence 5, Appl 43 83 3.3 933 US-08-293-728-2 Sequence 5, Appl 43 83 3.3 933 US-08-293-728-2 Sequence 2, Appl 44 83 3.3 933 US-08-293-728-2 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 65 82 US-07-642-734C-4 Sequence 2, Appl 65 82 US-07-642-734C-4 Sequence 4, Appl 65 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 86 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 65 86 83 3.3 3567 2 US-07-642-734C-4 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App. 41 83 3.3 417 5 PCT-US92-06965A-25 Sequence 20, App. 41 83 3.3 550 1 US-08-348-891A-5 Sequence 5, App. 42 83 3.3 550 2 US-08-93-788-2 Sequence 5, App. 43 83 3.3 933 4 US-08-293-728-2 Sequence 2, Appl. 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl. 45 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl. 45 83 3.3 933 4 US-09-421-868-2 Sequence 2, Appl. 45 83 3.3 933 4 US-09-7642-734C-4 Sequence 2, Appl. 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl. 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl. 500-20-20-20-20-20-20-20-20-20-20-20-20-2 | 3.3 3.4 3.5 3.3 Sequence 1.3, App. 3.3 3.3 4.35 1 US-08-484-105-12 Sequence 1.2, App. 38 83.5 3.3 4.37 4 US-08-867-611-20 Sequence 1.2, App. 41 83 3.3 417 5 PCT-US92-06965A-25 Sequence 2.0, App. 41 83 3.3 550 1 US-08-348-891A-5 Sequence 5, App. 41 83 3.3 550 2 US-08-93-88-2 Sequence 5, App. 42 83 3.3 550 2 US-08-905-817-5 Sequence 5, App. 42 83 3.3 933 4 US-08-293-728-2 Sequence 5, App. 44 83 3.3 933 4 US-09-421-868-2 Sequence 2, App. 44 83 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APPLICANT: Briggs, Stev | 33 85 3.3 550 4 US-09-230-944-20 34 84.5 3.3 767 1 US-08-467-77-8 35 84 3.3 541 4 US-08-467-77-8 36 84 3.3 541 5 PCT-US92-06965A-13 Sequence 8, Appl 37 83.5 3.3 435 1 US-08-484-106-12 38 83.5 3.3 435 1 US-08-484-106-12 39 83 3.3 437 1 US-08-867-611-20 40 83 3.3 3.417 4 US-08-867-611-20 41 83 3.3 550 1 US-08-948-195-2 42 83 3.3 550 1 US-08-348-91A-5 Sequence 12, Appl 42 83 3.3 550 2 US-08-948-195-2 43 83 3.3 550 2 US-08-948-195-2 Sequence 5, Appl 43 83 3.3 933 4 US-09-293-728-2 44 83 3.3 3550 2 US-08-293-728-2 45 83 3.3 3550 2 US-08-293-728-2 46 83 3.3 3550 2 US-08-293-728-2 Sequence 2, Appl 45 83 3.3 3550 2 US-08-293-728-2 46 83 3.3 3550 2 US-08-293-728-2 Sequence 2, Appl 45 83 3.3 3550 2 US-08-293-728-2 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 2, Appl 45 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 64 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 64 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 64 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 64 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 64 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 64 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 64 83 83 3.3 3567 2 US-07-642-734C-4 Sequence 4, Appl 64 83 83 3.3 3567 2 US-07-642-734C-4 Sequence 5, Appl 64 84 84 84 84 84 84 84 84 84 84 84 84 84 | 29 85 3.3 438 4 US-08-485-264A-105 Sequence 105. 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83 3.3 393 4 US-08-293-728-2 39 84 3.3 3.3 550 2 US-07-642-734C-4 39 83 3.3 350 2 US-07-642-734C-4 39 83 3.3 350 2 US-07-642-734C-4 39 83 3.3 350 2 US-07-642-734C-4 39 83 3.3 3567 2 US-07-642-734C-4 30 850 10 850 10 850 823-728-2 30 850 10 850 10 850 823-728-2 30 850 10 850 10 850 823-728-2 30 850 10 | 32 85 3.3 550 1 05.08 279 700.22 3 3 3 3 3 3 3 3 3 3 3 4 10 5 0 20 20 3 3 4 10 5 0 20 3 3 4 10 5 0 3 3 3 3 4 10 5 0 3 3 3 4 10 5 0 3 3 3 4 10 5 0 3 3 3 3 4 10 5 0 3 3 3 3 4 10 5 0 3 3 3 3 4 10 5 0 3 3 3 3 3 3 4 10 5 0 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 | 32 85 3.3 550 1 05.08 275-700.22 3equence 22, App. 34 84.5 3.3 501 1 05.08 275-700.22 3equence 27, App. 35 84.5 3.3 501 1 05.08 487-701.8 3equence 20, App. 35 84.5 3.3 501 1 05.08 487-701.8 3equence 8, App. 35 84.5 3.3 541 5 07.0928-70956A-13 3equence 12, App. 37 83.5 3.3 435 1 05.08 484-106-12 3equence 12, App. 39 83.5 3.3 435 1 05.08 484-106-12 3equence 20, App. 40 83 3.3 40.5 1 05.08 484-106-12 3equence 22, App. 41 83 3.3 550 2 05.08 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US-09-282-305-8
               RESULT 3
US-09-282-305-6
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US-09-282-305-8
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Best L
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Patent No. 6287843
Sequence 6, Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Malze Histone Deacetylases
FILE REFERENCE: 5718-44,
                                                                                                                                                                                                                     303
                                                                                                                                                                                                                                                                                     243
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                                                                                                                                                                                                                                                                                                        DGMDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLR
                                                                                                                                                                                                                                                                                                                                                                       VLYIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                     CRASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKWFKR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIQPKSVENLNTTKDLENIKNMILENLSKIEHVPSTQFHDRPSDPEAPEEKEEDMDKRPP 416
                                                                                                                SGTATYESDSDDDD 433
                                                                                                                                                                                  MENLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRV--LDEPEDDMETRPKPRXW 419
                                                                                                                                                                                                                   SFNVPLLLLLGGGGYTIRNVARCWCYETGVALGQEPEDKMPVNEYYEYFGPDYTLHVAPSN
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                                                                                   -----DSDMEVDD
                                                                                                                                                 MENKNTRQQLDDIRSKLLDNLSKLRHAPSVHFQERVPDTEIPEQDEDQDDPDERHDP---
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66,4%;
US/09282305
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Pred. No. 3.2e-163;
9; Mismatches 72;
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Sequence 1, Application US/08528255A
Patent No. 5659016
GENERAL INFORMATION:
APPLICANT: NAKAMURA, YUSUKE
APPLICANT: FURUKAWA, YOICHI
TITLE OF INVENTION: RPDL PROTEIN AI
TITLE OF INVENTION: ENCODING THE S.
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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GENERAL INFORMATION:
APPLICANT: Baldwin, Donald A.
APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
APPLICANT: Crane, Virginia C.
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Best Local Similarity
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PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 439
STREET: 2026 Rami
CITY: Kalamazoo
STATE: Michigan
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                        TATYESDSD---DDDKPL 436
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                                                      2026 Rambling
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                                                                                                                            : FURUKAWA, YOICHI
/ENTION: RPDL PROTEIN
/ENTION: ENCODING THE
                                                                           FLYNN,
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                                                                         THIEL, BOUTELL & TANIS,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: MS-DOS 5.0 SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
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LIBRARY: human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Terryence F. Chapman
REGISTRATION NUMBER: 32549
REFERENCE/DOCKET NUMBER: FY
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PRIOR APPLICATION DATA:
                                                                                                                                                                      304
                                                                                                                                                                                            316 TIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIR 375
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405 I ---- SICSSDKRIACEEEFSDSEEE 426
                                      436 LHGYSCRGGATTDRDSTGEDEMDDDNPE 463
                                                                                364 QRIFENLRMIPHAPGVQMQAIPE-DAIPEESGDE--
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                                                                                                                                                                                                                                                                                                                                                                                                                             124 LNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGV 195
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FILING DATE: 22-SEPTEMBER-1994
APPLICATION NUMBER: JP7-183763
FILING DATE: 20-JULY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 KYHSDDYIKFLRSIRPDNMSEYS--KQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 RFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVK 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 GRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIG 75
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                                                                                                                         NTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDDDDKP 435
                                                                                                                                                                 TIRNVARCRTYETAVALDTEIPNELPYNDYFEYFGPDFKLHISPSNMTNQNTNEYLEKIK 363
                                                                                                                                                                                                                                                                                                                                                              EEAFYITDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRP 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.9%; Score 1448.5; DB 1; Length 482; 58.3%; Pred. No. 7.6e-152; ative 79; Mismatches 81; Indels 27;
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                                                                                   DEDDPDKR 404
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 261;
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APPLICANT: NAKAMURA, YUSUKE
APPLICANT: : FURUKAWA, YOTO
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FILING DATE: 23-SEP-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/528 255
FILING DATE: September 14, 1995
APPLICATION NUMBER: 196-227896
PILING DATE: 22-SEPTEMBER: 1994
APPLICATION NUMBER: JPC-183763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: (
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REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
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MEDIUM TYPE: Diskette, 3.5 inches, 1.44 Mb storage
COMPUTER: IBM PC/XT/AT Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
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ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: ENCODING THE SAME
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                                                                                                                                                 124
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CITY: Kalamazoo
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                                                                                                                                                                                                                                                                                                                                       76 RFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLEDFCRASAGGSIGAAVK 135 ::|| :| : | : | : | : | : | : | | : | : | | : | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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EEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRP 255
                                                                                                                                             LNKQQTDIAVNWAGGLHHAKKSEASGFCYVNDIVLAILELLKYHQRVLYIDIDIHHGDGV 183
                                                                                                                                                                                                                        LNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGV 195
                                                                                                                                                                                                                                                                                                   KYHSDDYIKFLRSIRPDNMSEYS--KQMQRFNVGEDCPVFDGLFEFCQLSTGGSVASAVK 123
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7.6e-152;
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; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2
; SEQ ID NO 4
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Zea mays
US-09-282-305-4
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US-09-282-305-4
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Best Local Similarity
Matches 252; Conserv
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Patent No. 6287843
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases And Their Uses
FILE REFERENCE: 5718-44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/282,305
CURRENT FILLING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
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                                        358 DPSPMENLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRP--K 415
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                                                                                                     RFLRSYNVPLMVLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHV 357
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QPKSVENLNTTKDLENIKNMILENLSKIEHVPSTQFHDRPSDPEAPEEKEEDMDKRPPQR 311
                                                                                                                                                                  VPLSDGIDDTTFRGLFQCIIKKVMEVYQPDVVVLQCGADSLAGDRLGCFNLSVKGHADCL
                                                                                                                                                                                                        VPLNDGMDDESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCL 297
                                                                                                                                                                                                                                                FHRRVLYVDIDVHHGDGVEEAFFTTNRVMTVSFHKYGDFFPGTGHITDVGAAEGKHYALN 131
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                                                                                  RFLRSYNVPMMYLGGGGYTIRNVARCWCYETAVAVGVEPDNKLPYNDYYEYFGPDYTLHI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRRLEISRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDG 117
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US-09-282-305-10
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Matches
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APPLICANT: Briggs, Steven P.
APPLICANT: Crane, Virginia C.
TITLE OF INVENTION: Maize Histone Deacetylases
FILE REFERENCE: 5718-44,
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CURRENT FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: 60/080,563
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 18
SOFTWARF. PRIORIEM.
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TYPE: PRT
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mes 235; Conserv
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                                                           DND 426
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                                                                                                                                                                                                                                    NVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIRNTL 378
                                                                                                                                                                                                                                                                                         KVVETYLPGAIVLQCGADSLARDRLGCFNLSIEGHAECVKFVKKENIPLLVTGGGGYTKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVFEAF 199
                                                                                                                                       MESLRYIQHAPGVQMQEVPPDFYIPDFDEDELD--PDERVDQHTQDKQIHRDDEYYEGDN
                                                                                                                                                                                                                NVARCWAVETGYLLDTELPNEIPKNEYIEYFAPDYTLKVPNLNMDNLNSKTYLSSIKVQV
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                                                                                                                                                                                                                                                                                                                                                                     YFTDRVMTVSFHKYGDLFFPGTGDIKDIGEREGKYYAINIPLKDGIDDTSFTRPFKTIIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49.1%; Score 1249.5;
55.6%; Pred. No. 7.5e
tive 64; Mismatches
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nes 107;
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US-09-446-504-80

Sequence 80, Application US/09446504
Patent No. 6218150
GENERAL INFORMATION:

APPLICANT:
APPLICANT:

UEMORI, Takashi SATO, Yoshimi

TYPE: PRT

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APPLICANT: Gustafsson, Claes
APPLICANT: Betlach, Mary C.
APPLICANT: Abtley, Gary
APPLICANT: Julien, Bryan
APPLICANT: Jilien, Bryan
APPLICANT: Ziermann, Rainer
APPLICANT: Ziermann, Rainer
APPLICANT: Ziermann, Rainer
APPLICANT: Ziermann, Rainer
APPLICANTION: THEREFOR
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 30062-20020.20
CURRENT APPLICATION NUMBER: US/09/144,085
CURRENT FILING DATE: 1998-08-31
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CURRENT APPLICATION NUMBER: US/09/446,504
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: PCT/JP98/02845
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: JP 9-187496
PRIOR FILING DATE: 1997-06-26
PRIOR APPLICATION NUMBER: JP 9-320692
PRIOR FILING DATE: 1997-11-27
                                                                                                                                                                                                                                                                                                                                                                                                           US-09-144-085-2
EARLIER APPLICATION NUMBER: 09/010,809
EARLIER FILING DATE: 1998-01-22
NUMBER OF SEQ ID NOS: 8
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 2
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LENGTH: 335
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Best Local Similarity
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APPLICANT:
APPLICANT:
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SOFTWARE: Patentin Ve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --ALHYGGLHMALVRPPGHHAGRRGRAMGAPTLGFCIFNNAASAVVTLKEEGVGKVVVID 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YINFVKE-----AVEKGITRLD--PDTYVSPGTWSAALLALGAARSAALS----- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESFRSLFRPLIQKVMEVYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVP 306
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MUKAI, Hiroyuki
ASADA, Kiyozo
KATO, Ikunoshin
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Sequence 2, Application US/09428517

Patent No. 6251636

GENERAL INFORMATION:
APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert

APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 30062-20029.00

CURRENT APPLICATION NUMBER: US/09/428,517

CURRENT FILING DATE: 1999-10-28

EARLIER APPLICATION NUMBER: 60/120,254

EARLIER APPLICATION NUMBER: 60/120,254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-428-517-2
                                                                 EARLIER APPLICATION NUMBER: 60/106,100
EARLIER FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
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                          LENGTH: 4150
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1729 VAGLQR-----GEAVAADQVLKELGLDSLMAVALRNRLTSRTETSLPATLVFDY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1669 GLESSGELPALFRALLRPSLRKASSATRRDASALRERLSALPEAERLNALVELVRGEVAA 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1632 GFVPMPVEEGLALLDAALSRPEASLVPVH-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1515 AVLHLAGVLDDGVLTAQTAERLSRVLAPKVDGALHLHELTRELDLAAFVLFSSAAGTFGA 1574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1466 GLEAPG------ARELVQSLEELGAETVTVAACDVSKREEVARVLAGIDAARPLS 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   449 RD 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRFLRSYNVPLMVLGGEGYT IRNVARCWCYETAVAVGV-----EPDNKLPYNEYFEYFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDDDDKPLHGYSCRGGATTD
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20.18;
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Pred. No. 0.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -TLLEQLSGLIHA 388
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Gaps

18;

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OTHER INFORMATION: Description of Artificial Sequence: Recombinant
OTHER INFORMATION: Oleandolide PKS
US-09-428-517-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08296362
Patent No. 5691306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                         NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/296,362
FILING DATE: 25-AUG-1994
CLASSIFICATION: 435
                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Deehr, Manya S.
REGISTRATION NUMBER: 37,120
REFERENCE/DOCKET NUMBER: 69)
                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: METHODS OF DETECTION AND TREATMENT OF TITLE OF INVENTION: PROTEIN TRAFFICKING DISORDERS AND INCREASING TITLE OF INVENTION: PROTEIN PRODUCTION

NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Thomas, Dav
APPLICANT: Wada, Ikuo
                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1076 GVTSPEDLWRLLAAGED 1092
                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 6300 C
CITY: Seattle
STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             981 RAERIDPDRA-----FRDLG------FDSLTALELRDRLDTAL-----GLRLPS 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             941 HPRPADDTESG--TGRTEASPPRPHDVLHLVRSH--AAAVLG-------HS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             883 ALRRGRDEA -- RSLTEAVARLHLHGVPMDWTSVLGGDVSRVPLPTYAFQRESHWLPSGEA 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             823 VRFGDGIRALGKLGTGSFLEVGPDGVLTAMARACVTAAPEPGHRGEQGADADAHTALLLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189 VHHGDGVEE-----AFYTT--DRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVP 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity hes 76; Conserv
                                           TELEFAX: (206)
TELEX: 3723836
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 98104-7092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVQFQHTPP--VNRVLDEPEDDMETRPKPRXWSGTATYESDSDDDDKPLH--GYSCR--G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LNDGMDDESFRSLFRPLIQKVME-----
    CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6300 Columbia Center, 701 Fifth Avenue
                                                                   (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thomas, David Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
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24.0%;
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                                                                                                                             690066.401C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08867611 Patent No. 6172189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GUTIERREZ, ROBIN A
APPLICANT: LESNIEWSKI, RICHARD R
APPLICANT: STEWART, JAMES L
APPLICANT: RUPPRECHT, KEVIN R
TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
TITLE OF INVENTION: ANTIGENS
NUMBER OF SEQUENCES: 59
                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 MKETKLPGDKGLVLMSRAKHHAISAKLNKPFLFDTKPLIVQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 FGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRPLIQKVMEVYQPEAVVLQ 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 FQNGIECGGAYVKLLSKTPELNLDQFHDKTPYTIMFGPDKCGEDYKLHFIFRHKNPKTGV 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 PDEEATKPDGWLDDEPEYVPDPDAEKP 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 YEEKHAKRPDADLKTYFTDKKTHLYTLILNPDNSFEILVDQ--SIVNSGNLLNDMTPPVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 VAVGVE-----PD-----NKLPYNEYF--EYFGPDYTLHV---DPSPMENL 365
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                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 02-JUN-1997
                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                          STREET:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                      CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 FADSF-----IAKYDGKWEVDE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
                       FILING DATE:
                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TDRDSTGEDEMDDDNPE----PDVNPP 469
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                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESAI, SURESH N
CASEY, JAMES M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DAWSON, GEORGE J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAILEY, STEPHEN H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVARE,
                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.7%; Score 93; DB 1; Length 593; 21.4%; Pred. No. 0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUSHIL G
                                                                                                                             us/08/867,611
US/08/179,896
                                           US/08/646,757
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FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:

US 07/748,566

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

US 07/748,565

FILING DATE:

APPLICATION NUMBER: US 07/748,561 FILING DATE: 21-AUG-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 24-AUG-1990

US 07/572,822

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 07-NOV

07-NOV-1990

US 07/614,069

TELECOMMUNICATION INFORMATION: TELEPHONE: 708-937-6365

REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834.US.P6 NAME: POREMBSKI, PRISCILLA E REGISTRATION NUMBER: 33,207

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                                                                                                                                                                                                                                                            Sequence 7, Application PC/TUS9206965A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 708-937-9556
INFORMATION FOR SEQ_ID_NO: 2:
                                                                                                                      APPLICANT: DEVARE, S.
APPLICANT: DESAI, S.
APPLICANT: DAILEY, S.
APPLICANT: DAILEY, S.
TITLE OF INVENTION: HCV SYNTHETIC PEPTIDE FROM NS1 REGION
NUMBER OF SEQUENCES: 35
CORRESSPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            138 -- NPNAVKVVLDAEGYAL ----- YFSRATIPWDRDR--
                                                                                                                                                                                                                                                                                                                                                                                                   234 -- VDTPEDLDPSTNSMSTNPKPQ 254
                                                                                                                                                                                                                                                                                                                                                                                                                                             401 RVLDEPED-----DMETRPKPR 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 3.6%;
Local Similarity 22.4%;
                                       STREET: ONE ABBOT CITY: ABBOTT PARK STATE: ILLINOIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 GAERIIVATDHEDVARAVEAAGGEVCMTRADHQ-----SGTERLAEV-VEKCAFSDDTVI 94
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                    COUNTRY:
                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DPSPMENLNTPKDMERIRNTLLEQLSGLIHAPSVQF---QHTPPVN 400
60065-3500
                                                                                 E: ABBOTT LABORATORIES
ONE ABBOTT PARK ROAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -MLEQLRVLWYGEKIHVAVAQEVPGTG 233
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Query Match
Best Local Similarity
watches 59; Conserva
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US-08-291-896-2
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                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 708-937-6365
TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 7:
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 820 amino acid
                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
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CURRENT APPLICATION DATA:
PCT/US92/06965A
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release ""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 YGYRAGFIRRYVNWQPSPLEHIE----
                                                                            APPLICATION NUMBER: US/08/291,896 FILING DATE: 17-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1 CLASSIFICATION:
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22.4%; Pred. No.
                                                                                                                                                                                                                                                              DNA fragment carrying the gene encoding the enzyme for fragmenting N-acetylheparosan and the adjacent sequences permitting its expression, recombinant enzyme intended for fragmenting N-acetylheparosan and its use.
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                                                                                                                                          Version
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Best Local Similarity 19.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ledoux, recombinant enzyme intended for fragmenting N-acetylheparosan
                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION MADER: US/08/485,278
FILING DATE: 07-JUN-1995
                FILING DATE: 17-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,4
                                                                                               FILING DATE: 17-AUG-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9:
FILING DATE: 17-AUG-1993
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ZIP: 200
                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version
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STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                   CLASSIFICATION:
  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SQNTLIDGVIARNYPQFGAVELKTAAKYNIVSNVIGEECQHVVYNGTE--TETAPTNNII 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYTLHVDPSPMEN------LNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGGEGYTIRNVARCWCYETAVAVGVEPDNKLP-----YNEYFEY-----FGP 351
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P58114NA
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Best Local Similarity
Matches 69; Conserv
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TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                         296
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                                                                                                                                                                                                                                                                                                                                                                                                                                      163 YVDAAIAGVIGGFGWF------IQYGSG---AVYRT-----FQDKMRDGVSI 200
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                                         DEPEDDMETRPKPRX---WSGTATYESD----SDDDDKPLHGYSCRG 443
                                                                                                                             DYTLHVDPSPMEN-----LNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRVL 403
                                                                                                                                                                         SGGHDVSVKNIRFTNTRGPGFSLIAYPDNGIPSGYIVRDIRGEYLGFANNKKAGCVLFDS
                                                                                                                                                                                                                                                             GTGGGTIKQYDRDGNHLVFNMPDGGMLSTLTIMGNKSDDSVQGH-------QVSF 295
                                                                                                                                                                                                                                                                                                                                               KDFGAQNG-----ILNDNKD-----AFTKSLHSFSSVFVPEGVFNTSLVSLSRCGLY 247
                                                                                                                                                                                                                  LGGEGYTIRNVARCWCYETAVAVGVEPDNKLP-----YNEYFEY-----FGP
                                                                                                                                                                                                                                                                                                    SLSG------DRLG---CFNL------SVKGHADCLRFLRSYNVPLMV 309
SSV---MANNPKYAAVVVGKGTGNLISDVLVDYSESDAKQAHGVTVQG
                                                                                  SQNTLIDGVIARNYPQFGAVELKTAAKYNIVSNVIGEECQHVVYNGTE--TETAPTNNII 413
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17;

Search completed: April 26, 2002, 17:51:27 Job time: 35 sec

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Minimum DB seq
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s thali	AAG51592	21	468	11.4	289	•
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Maize histone	AAY28801		432	9.	1249.5	٠.
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e histone deac	AAY58828	21	493	æ	1498	_
e histone dea	AAY28799	20	439	59.7	1520	~
Maize histone deac	AAY28800	20	517		1551.5	٠

ALIGNMENTS

RESULT AAB67812 elongation), comprises Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl Miki B, CA2316036-A1 Arabidopsis thaliana Histone deacetylase; AtRPD3B; RPD3; gene expression; transgenic plant; Amino acid sequence of a histone deacetylase designated AtRPD3B 29-JUN-2001 (first entry) AAB67812; AAB67812 standard; N-PSDB; (MIAC) 27-AUG-1999; 24-AUG-2000; 2000CA-2316036. 27-FEB-2001. HDA1; ethylene-responsive phenotype; 2001-258457/27. DB; AAF80351. CANADA MIN AGRIC & AGRI-FOOD CANADA Brown D, Tian L, 99US-0383971. Protein; introducing genes encoding histone deacetylase Š 471 <u>.</u> ₹ hypocotyl elongation

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Best Local
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   Arabidopsis thaliana
                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 1499.
                                                                                   17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                      termination sequence
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09-MAR-1999;
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                                                                                                                     Arabidopsis thaliana.
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Best Local
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                                        N-PSDB;
                                                                                                                                                                                                                          disease response
                                                                                                                                                                                                                                                                                                13-JAN-2000 (first entry)
         New deacetylase genes, used for producing transgenic plants which increased disease resistance
                                        WPI; 1999-611038/52
N-PSDB; AAX90837.
                                                                       Baldwin DA,
                                                                                                                   03-APR-1998;
                                                                                                                                       02-APR-1999;
                                                                                                                                                                                                                                                                                                                                         AAY28797 standard; protein; 458
                                                                                                                                                            14-OCT-1999
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                                                                                            (PION-) PIONEER HI-BRED
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                                                                                                                                                                                                                                                                                                                                                                                                                                      eddmetrpkpriwsgtatyesdsddddkplhgyscrggattdrdstgedemdddnpepdv 420
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                                                                                                                 98US-0080563
                                                                                                                                       99WO-US07370
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99.5%;
                                                                                              INT INC.
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Pred. No. 7
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Additionally, compositions find use in screening for toxins that affect pathogenicity and in determining which disease response promoters are regulated by histone deacetylase.
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                               24 - AUG - 2000;
                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                        Histone deacetylase; AtRPD3A; RPD3; gene expression; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB67811 standard; Protein;
                                                                                                  27-FEB-2001
                                                                                                                                                                                                                                                                                                    HDA1; ethylene-responsive phenotype; hypocotyl elongation
                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a histone deacetylase designated AtRPD3A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          designated AtrPDJA. The protein is homologous to yeast RPDJ and HDA1. The polynucleotide sequence is used in the method of the invention. The specification describes a method for regulating gene expression in transgenic plants. The method comprises modifying histones by introducing chimeric nucleotide sequences which have regulatory elements in operative ensociation with a gene of interest or with a nucleotide sequence encoding histone deacetylase. The method is useful for regulating the developmental, physiological or biochemical pathway within a plant, particularly for repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation). The method is also useful as a functional test for identifying a phenotype associated with perturbing a gene. The histone deacetylase genes are useful for altering the development of an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Methods for regulating gene expression in transgenic plants, e.g. repressing ethylene-responsive phenotypes (e.g. inhibition of hypocotyl elongation), comprises introducing genes encoding histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10;
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473 p 473
                           462 P
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                                                                                                                                                                                                                                                                                                                                                124 ASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVL 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 DESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEI 63
                                                                                                                                                                                                                                                                                 ----dmdvdddrkpipsrvkreavepdtkdkdglkgimergkgcevevdesgstkvtgvn
                                                                                                                                                     nvpllllggggytirnvarcwcyetgvalgvevedkmpeheyyeyfgpdytlhvapsnme
                                                                                                                                                                                                                            SRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCR 123
                                                                                                      nknsrqmleeirndllhnlsklqhapsvpfqerppdtetpevdedqedgdkrwdpds---
                                                                                                                      NLNTPKDMERIRNTLLEQLSGLIHAPSVQFQHTPPVNRV--LDEPEDDMETRPKPRXWSG
                                                                                                                                                                                       NVPLMYLGGEGYTIRNVARCWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPME 363
                                                                                                                                                                                                          iddesyhllfkpimgkvmeifrpgavvlqcgadslsgdrlgcfnlsikghaecvkfmrsf
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                                                                                                                                                                                                                                                                                                                       tyaggsvggsvklnhglcdiainwagglhhakkceasgfcyvndivlailellkqhervl
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                                                                                                                                                                                                                                                                                                                                                                                                                               dtggnslasgpdgvkrkvcyfydpevgnyyyggghpmkphrirmthallahygllqhmqv 61
                           462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 1A; 91pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents Arabidopsis thaliana histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0383971.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tian L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61.4%; Score 1561.5; DB 2 60.7%; Pred. No. 5.8e-158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Mismatches
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                                                                              -LHGYSCRG-GATTDRDSTGEDEMDDDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length
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        iddesyhllfkpimgkvmeifrpgavvlqcgadslsgdrlgcfnlsikghaecvkfmrsf
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suppressing expression of selected gene for treating cancer, involves introducing peptide comprising nucleic acid binding portion that binds to or associated with selected gene and chromatin inactivation portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB67165 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-138069/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Buluwela L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W0200102019-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis histone deacetylase 1 HDAC1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Local Similarity 60.7 tes 292; Conservative
                                                                                                                                                                                                                           ASAGGSIGAAVKLNRQDADIAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVL 183
                                                                                                                                                                                                                                                                                                    SRPSLADASDIGRFHSPEYVDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCR 123
                                                                                                                                                                                                                                                                                                                                                                                                     DESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRRLEI 63
                                                                                                                          YIDIDVHHGDGVEEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDG
                                                                                                                                                                            tyaggsvggsvklnhglcdiainwagglhhakkceasgfcyvndivlailellkghervl
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60.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1561.5; DB 22; Pred. No. 5.8e-158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .8e-158;
es 94;
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RESULT 11
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Matches 290;
                                                                                                                                                        plant histone deacetylases. The invention relates to isolated rice, soybean and wheat nucleic acid fragments encoding HDL. It also relates to the construction of a chimeric gene encoding all a portion of HDL, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of HDL in a transformed host cell. The availability of
                                                                                                             nucleic acid sequences encoding (portions) of histone deacetylase proteins will facilitate studies of global transcriptional regulation in eukaryotic cells, and will also provide mechanisms
                                                                       Sequence
                                                                                                   control transcriptional gene regulation in plants
                                                                                                                                                                                                                                                 (HD1), a chromatin associated protein, as deduced from a soybean root cDNA clone (see AAZ58260) isolated on the basis of homology \,
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ58260.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromatin associated protein; histone deacetylase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soybean histone deacetylase 1 (HD1) protein.
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                                                                                                                                                                                                                                                                              The present sequence is that of soybean histone deacetylase 1
                                                                                                                                                                                                                                                                                                                                         transforming plants
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               Local Similarity
                                                                                                                                                                                                                                                                                                                                                       nucleic acid fragment useful as
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                                                                                                                                                                                                                                                                                                                                                                                                                               RE,
                                                                                                                                                                                                                                                                                                            Page 27-28;
                                                                         473 AA;
Conservative
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             61.3%; Score 1558.5; DB 21; 61.8%; Pred. No. 1.1e-157;
                                                                                                                                                                                                                                                                                                           36pp; English.
71;
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83;
Indels
                             Length 473;
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RESULT 1
AAY28800
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maize histone deacetylase; HD; HD cDNA; family 1, ZmHD1; gene repression; acetyl modification; promoter; regulatory element; transgenic plant; disease resistance; toxin screening; pathogenicity;
      Claim
                                                                                                                                                                                                                                              03-APR-1998;
                                                                                                                                                                                                                                                                                     02-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                              disease response promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maize histone deacetylase-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY28800 standard;
                                       New deacetylase genes, used for producing transgenic increased disease resistance
                                                                                                     N-PSDB; AAX90840
                                                                                                                          WPI; 1999-611038/52
                                                                                                                                                               Baldwin DA, Briggs
                                                                                                                                                                                                      (PION-) PIONEER HI-BRED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DESGISLPSGPDGRKRRVSYFYEPTIGDYYYGQGHPMKPHRIRMAHSLIIHYHLHRKLEI 63
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1; Page 63-65; 87pp; English.
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belonging to family 1, ZmHD1. The modifications, may be localised

The present sequence is maize histone deacetylase encoded by HD cDNA

This enzyme responsible d to promoters targeted

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Best Local
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                                                                                                                                                                                acetyl modification; promoter; regulatory element;
disease resistance; toxin screening; pathogenicity;
disease response promoter.
                                                                                                                                                                                                                                                                                                13-JAN-2000
                                                                                                                                                                                                                                                                                                                                                            AAY28799 standard;
                                                                                                                                                                                                                                   Maize histone deacetylase; HD;
(PION-) PIONEER HI-BRED INT INC
                              03-APR-1998;
                                                                                                                                                        Zea mays
                                                                                                                                                                                                                                                                 Maize histone deacetylase-3.
                                                             02-APR-1999;
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                                                             99WO-US07370.
                                                                                                                                                                                                                                                                                                                                                           protein; 439
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66.4%;
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Pred. No. 7.2
                                                                                                                                                                                                                  HD cDNA; family 1, ZmHD1; gene repression;
regulatory element; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Best Local
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                                                                                                                                  AAY58828 standard; Protein; 493
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                                                                                                                                                                                                                                                                                                                                                  439 AA;
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Chromatin associated protein; histone deacetylase rice; transgenic plant; transcription regulation.

Rice histone deacetylase 1 (HD1) protein (C-terminal portion).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 VDFLASVSPESMGDPSAARNLRRFNVGEDCPVFDGLFDFCRASAGGSIGAAVKLNRQDAD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 YEYEPTIGDYYYGOGHPMKPHRIRMAHSLIIHYHLHRRLEISRPSLADASDIGRFHSPEY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 yfydaevgnyyyggghpmkphrirmthallahygildqmqvlkphpardrdlcrfhaddy 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocal Similarity
sklrhapsvqfqerpp-eaelpeqdedqed-pder---
                                                                                                                                                                                                                       IAINWGGGLHHAKKSEASGFCYVNDIVLGILELLKMFKRVLYIDIDVHHGDGVEEAFYTT 202
                                                          SGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSD---DDDKPLHGY 439
                                                                                                                                                                   CWCYETAVAVGVEPDNKLPYNEYFEYFGPDYTLHVDPSPMENLNTPKDMERIRNTLLEQL
                                                                                                                                                                                                                                                                                  VYQPEAVVLQCGADSLSGDRLGCFNLSVKGHADCLRFLRSYNVPLMVLGGEGYTIRNVAR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-182439/16
                                                                                                           \verb|cwcyetgvalgheltdkmppneyfeyfgpdytlhvapsnmenkntrqqlddirsrlldnl|\\
                                                                                                                                                                                                                                                                                                                                      drvmtvsfhkfgdyfpgtgdirdighskgkyyslnvplddgiddesyqslfkpimgkvme
                                                                                                                                                                                                                                                                                                                                                                                                                                                     iainwagglhhakkceasgfcyvndivlailellkyhgrvlyvdidihhgdgveeafytt 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ÆE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ58259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vollmer SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0092841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US15807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.9%; Score 1498; DB 21; 64.4%; Pred. No. 3.5e-151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
  ----hhadsdvemddvkpldds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 18; Gaps
                                                                                                                                                                      382
                                                                                                                                                                                                                             297
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                                                                                                                                                                                                                     influencing cell cycle progression or to modulate gene transcription. The products can be used for diagnosis and therapy. They can be used, for example, to treat tumours or proliferative disorders or spermatogenesis, osteogenesis, chondrogenesis or the differentiation of progenitor cells. They can also be used to treat psoriasis, bone diseases, they can also be used to treat psoriasis, bone diseases, or for repair of cartilage, increasing bone density, liver repair subsequent to a partial population, increasing bone density, liver repair subsequent to a partial population of the property of the property of the processing bone density.
                                                          also be used in cell cultures.
note: in the claims, the full length HDl sequence is
referred to as SEQ. ID. No.2; from the disclosure it
                                                                                                                                         hepatectomy, to promote regeneration of lung tissue in the treatment of emphysema, or for inducing tolerance in autoimmune diseases, and transplant recipients. HDx inhibitors can be used as anti-fungal agents, preservatives in foodstuff, feed supplements for promoting weight gain i
                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide, designated HD1. The HDx polypeptides are capable of modulating proliferation survival and differentiation of cells. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Pages 112-114; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated histone deacetylase polypeptide(s) and genes - used to develop products for modulating the proliferation, survival or differentiation of cells, e.g. for treating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Histone deacetylase gene; HDx; HDl; HDx polypeptide; deacetylation; H3 H4; cell differentiation; chromatin structure; cell cycle progression; proliferative disorder; fibroproliferative disorder;
                                                                                                                                                                                                                                                                                                                                                                     proteins are able to alter chromatin structure by deacetylating histones such as H3 or H4. They have the ability to modulate cell growth by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel histone deacetylase (HDx) protein, designated HD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW29324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW29324 standard;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a novel histone deacetylase (HDx)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hassig CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09735990-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               degenerative disorder; autoimmune disease; HDx inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-APR-1998 (first entry)
                                                                                                                      livestock, disinfectants, insecticides or defoliants. The products can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HARD ) HARVARD COLLEGE
                                      is SEQ. ID. No.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 SCRG----GATTDRDSTGEDEMDDD 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              409 grrssignvrvkresaetdaadqd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1997-489651/45.
  482 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jamison TF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0624735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-US05275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schreiber SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taunton
                                                            is clear that HD1
                                                                               incorrectly
                                                                                                                                              'n
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Query Match Best Local Similarity

57.5%; Score 1462.5; DB 1 58.5%; Pred. No. 2.2e-147;

DB 18; Length 482;

Matches 262;

Conservative

79;

Mismatches

80;

Indels

27;

Gaps

4.

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			7
	LHGYSCRGGATTDRDSTGEDEMDDDNPE 463	436	γ
404	grlfenlrmlphapgvgmgaipe-daipeesgdededdpdkr 404	364	DЬ
435	NTLLEQLSGLIHAPSVQFQHTPPVNRVLDEPEDDMETRPKPRXWSGTATYESDSDDDDKP 435	376	VΩ
363	tirnvarcwtyetavaldteipnelpyndyfeyfgpdfkihispsnmtngntneylekik	304	Dδ
375		316	Qγ
303	vmskvmemfqpsavvlqcgsdslsgdrlgcfnltikghakcvefvksfnlpmlmlggggy 303	244	Ъ
315	LIQKYMEYYQPEAVYLQCGADSLSGDRLGCFNLSYKGHADCLRFLRSYNVPLMYLGGEGY	256	Qy
243		184	Ъ
255	EEAFYTTDRVMTVSFHKFGDFFPGTGHIRDVGAEKGKYYALNVPLNDGMDDESFRSLFRP	196	ΟУ
183	lnkqqtdiavnwagglhhakkseasgfcyvndivlailellkyhqrvlyididihhgdgv 183	124	Db
195		136	Ŷ
123	kyhsddyikflrsirpdnmseyskqmqrfnvgedcpvfdglfefcqlstggsvasavk 123	66	Ф
135	REHSPEYVDFLASVSPESMGDPSAARNLRRENVGEDCPVFDGLFDFCRASAGGSIGAAVK 135	76	Qy
65	gtrrkvcyyydgdvgnyyyggghpmkphrirmthnlllnyglyrkmeiyrphkanaeemt	6	Вb
75		16	Ŷ

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